

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 20, 2006, 22:15:21 ; Search time 195 Seconds
(without alignments)
898.020 Million cell updates/sec

Title: US-10-056-405-2

Perfect score: 1973
Sequence: 1 MVINPKVKFKCAPIKNGKTLT.....ADVFTRDITDQASVDFE 383Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1973	100.0	383	5	ABP52833
2	1973	100.0	383	7	ABR84476
3	1384	70.1	364	4	ABB61736
4	1384	70.1	364	8	ADO89588
5	1023	51.8	398	7	ABR84484
6	1002	50.8	470	4	ABB58174
7	982.5	49.8	401	4	ABBE1964
8	907.5	46.0	410	4	AAAG67780
9	903.5	45.8	418	4	AAAG67778
10	903.5	45.8	452	5	ABG69495
11	900.5	45.6	418	5	ABG70174
12	900.5	45.6	418	8	ADQ89786
13	897.5	45.5	418	4	AAAG67779
14	890	45.1	369	4	ABG13574
15	885	44.9	382	4	AAAG67785
16	885	44.9	409	4	AAAG67781
17	885	44.9	409	7	ADBS8179
18	885	44.9	409	7	ADBS8179
19	885	44.9	409	9	ADBN5251
20	885	44.9	479	10	ADBN5251
21	885	44.9	492	10	ADBN5251
22	885	44.9	492	10	ADBN5251
23	880	44.6	409	4	AAAG67784

24	874	44.3	360	6	ADA00635	ADA00635 Human bet
25	874	44.3	495	5	ADA00637	ADA00637 Human bet
26	869.5	44.1	410	5	ABG69496	ABG69496 Rat bait
27	869.5	44.1	410	7	ADBS8177	ADBS8177 Rat prote
28	869.5	44.1	410	7	ADBS8181	ADBS8181 Rat prote
29	869.5	44.1	526	8	ADR23187	ADR23187 Yellow flu
30	869.5	44.1	526	8	ADR23188	ADR23188 Green flu
31	869.5	44.1	526	8	ADR23186	ADR23186 Yellow flu
32	865	43.8	454	8	ADN24049	ADN24049 Bacterial
33	796.5	40.4	382	9	ADY65950	ADY65950 S. mansoni
34	780.5	39.6	388	4	AAAG67783	AAAG67783 Amino aci
35	780.5	39.6	388	4	ADX07504	ADX07504 Cyclin-de
36	780	39.5	405	4	AAW78763	AAW78763 Human pro
37	779.5	39.5	388	4	AAAG67782	AAAG67782 Amino aci
38	767.5	38.9	394	4	AED51702	AED51702 Pig arres
39	761	38.6	405	8	ADQ14327	ADQ14327 Human ret
40	761	38.6	405	8	ADRA1708	ADRA1708 Protein s
41	761	38.6	405	9	ABR77788	ABR77788 Human ret
42	723	36.6	405	9	AED51704	AED51704 Pig S-ant
43	661	33.5	468	4	AAW79747	AAW79747 Human pro
44	516.5	26.2	182	7	ADD27419	ADD27419 Human pro
45	516.5	26.2	182	7	ADD27127	ADD27127 Human adi

ALIGNMENTS

RESULT 1
ABP52833
ID ABP52833 standard; protein; 383 AA.
XX
AC ABP52833;
XX
DT 01-NOV-2002 (first entry)
XX
DE Anopheles gambiae arreslin 1 protein SEQ ID NO:2.
XX
KW Anopheles gambiae; mosquito; olfactory gene; arreslin 1; pest control;
XX odourant receptor; olfaction.
XX
OS Anopheles gambiae.
XX
PN WO200259274-A2.
XX
PD 01-AUG-2002.
XX
PF 28-JAN-2002; 2002WO-US002549.
XX
PR 26-JAN-2001; 2001US-0264649P.
XX 24-JAN-2002; 2002US-00056405.
XX
(UYVA-) UNIV VANDERBILT.
XX
Zwiebel LJ;
XX
WPI: 2002-627421/67.
XX N-PSDB; ABQ75102.
XX
PT New mosquito olfaction polypeptides and polynucleotides, useful for
PT mosquito management, i.e. controlling the pest and disease vectors, or
PT for identifying pest control agents.
XX
PS Claim 18; Fig 2; 96pp; English.
XX
XX
XX The present invention describes a purified Anopheles gambiae olfaction
XX polypeptide comprising a 383, 394, 380, 411, 412, 391, 157 or 401 residue
XX amino acid sequence (see ABP52833 to ABP52840) (S1), a conservatively
XX modified amino acid sequence of them, or a sequence of (S1) with at least
XX 20 consecutive residues. Also described: (i) an isolated polynucleotide
XX comprising: (a) a nucleotide sequence encoding the purified Anopheles
XX gambiae olfaction polypeptide; or (b) a nucleotide sequence that
XX hybridises under stringent conditions to a hybridisation probe comprising
XX a 1964, 1239, 1142, 1236, 1194, 1176, 474 or 1206 nucleotide sequence

CC (see AB075102 to AB075105 and AB075110 to AB075113) (S2), or its
 CC complement; and (2) a method for identifying an agent that binds to
 CC mosquito olfaction molecules comprising: (a) providing an isolated
 CC mosquito olfaction molecule; (b) contacting a test agent with the
 CC isolated mosquito olfaction molecule; and (c) detecting specific binding
 CC of the test agent to the isolated mosquito olfaction molecule, where the
 CC presence of specific binding identifies the test agent as a mosquito
 CC olfaction-binding compound. The mosquito olfaction molecules are useful
 CC for mosquito management, i.e. controlling this pest and disease vector. A
 CC method from the present invention of screening for substances that
 CC modulate arrestin-odorant receptor interaction is useful for identifying
 CC pest control agents. The present sequence represents Anopheles gambiae
 CC arrestin 1 from the present invention
 XX

Sequence 383 AA:

Query Match 100.0%; Score 1973; DB 5; Length 383;
 Best Local Similarity 100.0%; Pred. No. 3,9e-197;
 Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVYVFKYFKKCAPNGKVTLYMGRDPVHVSVEPIDIGIVLDEYIRDNKRVFGQIVCS 60
 DB 1 MVYVFKYFKKCAPNGKVTLYMGRDPVHVSVEPIDIGIVLDEYIRDNKRVFGQIVCS 60
 QY 61 FRYGREDEVMGLNFOKELCLASEQIYPRPEKSDKEQTKLQERLLKXGSAIIPFTNIS 120
 DB 61 FRYGREDEVMGLNFOKELCLASEQIYPRPEKSDKEQTKLQERLLKXGSAIIPFTNIS 120
 QY 121 PNAASSVTLLQGEDNDGPGCVSYVYKIFAGESETDTRHRSYVTLGIRKIQFAPTKQGQ 180
 DB 121 PNAASSVTLLQGEDNDGPGCVSYVYKIFAGESETDTRHRSYVTLGIRKIQFAPTKQGQ 180
 QY 181 QPCTLVKRDPMLSGSELELEVTLDKQYLHGERIGVNICIRNNSKNKWKIKKAWVQGVND 240
 DB 181 QPCTLVKRDPMLSGSELELEVTLDKQYLHGERIGVNICIRNNSKNKWKIKKAWVQGVND 240
 QY 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKQRGIALDGOIKRQDQ 300
 DB 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKQRGIALDGOIKRQDQ 300
 QY 301 CLASTTLLAQPDPQDARFVGIISYAVKVKLFLGALGELSABLPLVLMHPKPGTKAKVIHA 360
 DB 301 CLASTTLLAQPDPQDARFVGIISYAVKVKLFLGALGELSABLPLVLMHPKPGTKAKVIHA 360
 QY 361 DSQADVETFRQDTIDQASVDPE 383
 DB 361 DSQADVETFRQDTIDQASVDPE 383

RESULT 2

ABR84476 standard; protein; 383 AA.

ABR84476;

15-JAN-2004 (first entry)

Mosquito olfaction molecule, arrestin 1.

Arrestin 1; mosquito; olfaction; insecticide; antimalarial.

Anopheles gambiae.

MO2003076590-A2.

18-SEP-2003.

10-MAR-2003; 2003MO-US007174.

08-MAR-2002; 2002US-00094240.

(UYVA-) UNIV VANDERBILT.

XX

PI Zwiebel LJ;

XX WPI; 2003-722331/68.

DR N-PSDB; ACFT9716.

PT New mosquito arrestin 1 and 2 genes and polypeptides, useful for
 PT identifying mosquito olfaction molecule binding compounds which reduce
 PT the ability of mosquitoes to locate sources of bloodmeal, e.g. humans.

XX Claim 1; Fig 2; 101pp; English.

PS The present sequence is the protein sequence of arrestin 1, a novel
 CC mosquito olfaction molecule. The invention provides 9 novel mosquito
 CC polypeptides and the nucleic acids encoding them. These are arrestins 1
 CC and 2 and odorant receptor molecules 1-7. The odorant receptors function
 CC in a ligand-induced signal transduction pathway for the activation of
 CC mosquito olfaction. Arrestin functions to inhibit the activated signal
 CC transduction cascade. Thus, the odorant receptors act as an 'on' switch,
 CC and arrestin as an 'off' switch for the odorant detection system of the
 CC mosquito. Methods are provided for identifying compounds that interfere
 CC with the operation of the mosquito olfactory system, particularly
 CC compounds that modulate arrestin 2 activity. These are useful for the
 CC control of mosquitoes, particularly by reducing their ability to locate
 CC sources of bloodmeal

Sequence 383 AA:

Query Match 100.0%; Score 1973; DB 7; Length 383;
 Best Local Similarity 100.0%; Pred. No. 3,9e-197;
 Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVYVFKYFKKCAPNGKVTLYMGRDPVHVSVEPIDIGIVLDEYIRDNKRVFGQIVCS 60
 DB 1 MVYVFKYFKKCAPNGKVTLYMGRDPVHVSVEPIDIGIVLDEYIRDNKRVFGQIVCS 60
 QY 61 FRYGREDEVMGLNFOKELCLASEQIYPRPEKSDKEQTKLQERLLKXGSAIIPFTNIS 120
 DB 61 FRYGREDEVMGLNFOKELCLASEQIYPRPEKSDKEQTKLQERLLKXGSAIIPFTNIS 120
 QY 121 PNAASSVTLLQGEDNDGPGCVSYVYKIFAGESETDTRHRSYVTLGIRKIQFAPTKQGQ 180
 DB 121 PNAASSVTLLQGEDNDGPGCVSYVYKIFAGESETDTRHRSYVTLGIRKIQFAPTKQGQ 180
 QY 181 QPCTLVKRDPMLSGSELELEVTLDKQYLHGERIGVNICIRNNSKNKWKIKKAWVQGVND 240
 DB 181 QPCTLVKRDPMLSGSELELEVTLDKQYLHGERIGVNICIRNNSKNKWKIKKAWVQGVND 240
 QY 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKQRGIALDGOIKRQDQ 300
 DB 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKQRGIALDGOIKRQDQ 300
 QY 301 CLASTTLLAQPDPQDARFVGIISYAVKVKLFLGALGELSABLPLVLMHPKPGTKAKVIHA 360
 DB 301 CLASTTLLAQPDPQDARFVGIISYAVKVKLFLGALGELSABLPLVLMHPKPGTKAKVIHA 360
 QY 361 DSQADVETFRQDTIDQASVDPE 383
 DB 361 DSQADVETFRQDTIDQASVDPE 383

RESULT 3

ABB61736 standard; protein; 364 AA.

ABB61736;

26-MAR-2002 (first entry)

Drosophila melanogaster polypeptide SEQ ID NO 12000.

Drosophila; developmental biology; cell signalling; insecticide;

pharmaceutical.

XX

OS Drosophila melanogaster.
 XX WO200171042-A2.
 XX 27-SEP-2001.
 XX 23-MAR-2001; 2001WO-US0092231.
 XX 23-MAR-2000; 2000US-0191637P.
 XX 11-JUL-2000; 2000US-00614150.
 XX (PEKE) PE CORP NY.
 XX Venter JC, Adams M, Li PMD, Myers EW;
 XX WPI, 2001-656860/75.
 XX N-PSDB; ABL05839.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 PS
 XX Disclosure; SEQ ID NO 12000; 21pp + Sequence listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signaling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-ABL16175) and the encoded proteins (ABBS7737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 364 AA;

Query Match 70.1%; Score 1384; DB 4; Length 364;
 Best Local Similarity 70.3%; Pred. No. 1.8e-135;
 Matches 258; Conservative 51; Mismatches 54; Indels 4; Gaps 2;

QY 1 MYNNKRVFKKCAPNGKVTLYMGKRPVDVSGVEPIDGIVLVDDEYIRNKRFGQIVCS 60
 DB 1 MYNNKRVFKKCSPPNMNITLYMNRDPVDVSGVEPIDGIVLVDDEYIRNKRIFVQLVGN 60
 QY 61 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTLQERLLKLGSNAPFTFNIS 120
 DB 61 FRYGREDEDMIGLRPQKELTLVSQVCP-PQKODIQLTMQERLLKLGSNAPFTFMQMP 119
 QY 121 PNAPSSVTLQOGEDNDGDCGVSYVVKIFAGESETDRTHRSSTVTLGIRKIOFAPTKQG 180
 DB 120 PSSPASVVLQOKASDESQPCGVQYFVKIFGTGSDCDRSHRSSTINLGIRKVOYAPTKQGI 179
 QY 181 QGCTLVKRDPMSPGELSEVTLDKQLYHGERIGVNICIRNNSNMVKYKIKAMVOQGVND 240
 DB 180 QGCTVVRKDFLSPGELSEVTLDKQLYHGERIGVNICIRNNSNMVKYKIKAMVOQGVND 239
 QY 241 VVLFONGSYRNTVASLETSEGCPIOPGSSLOKVMYTLPLSSNKORRGIALDGOIKRQDO 300
 DB 240 VVLFONGGFRNTIATMETSEGCPLNPSSLOKVMYVPTLVANCDRAGIAVGDGIKRXDT 299
 QY 301 CLASTTLLAOPDORDAFGVIIISYAVVKVFLGALGELSABELPFVIMHPKPGTKAKVITHA 360
 DB 300 ALASTTLLASQARDAFGIIVSYAVVKVFLGALGELCAELPFILMHPKPSRKQQL--- 356
 QY 361 DSOADVE 367
 DB 357 EAGSIE 363

RESULT 4
 AD089588
 ID AD089588 standard; protein; 364 AA.

XX
 AC AD089588;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 XX Antagonist of cell cycle progression polypeptide #9.
 XX
 DE
 XX
 XX Cycostatic; cancer; cell division cycle; mitosis; meiosis;
 XX cell cycle progression.
 XX
 XX Drosophila melanogaster.
 XX
 XX WO2004063362-A2.
 XX
 XX 29-JUL-2004.
 XX
 XX 31-DEC-2003; 2003WO-GB005635.
 XX
 XX 10-JAN-2003; 2003US-0439123P.
 XX 06-MAY-2003; 2003US-0468402P.
 XX
 XX (CYCL-) CYCLACEL LTD.
 XX
 XX Glover D, Bell G, Frenz L, Midgley C;
 XX
 XX WPI, 2004-544089/52.
 XX N-PSDB; AD089587.
 XX
 PT New cell cycle progression genes and proteins for modulating cell cycle
 PT progression in cells, for preventing, treating or diagnosing cell
 PT proliferative diseases (e.g. cancer) or for identifying modulators of
 PT mitosis or meiosis.
 XX
 XX Claim 2; SEQ ID NO 18; 461pp; English.
 PS
 CC The present invention relates to a polynucleotide for preventing,
 CC treating or diagnosing a disease in an individual. The composition or the
 CC polypeptide, polynucleotide or RNA precursor, or antibody is useful for
 CC diagnosing, preventing or treating diseases (e.g. cell proliferative
 CC diseases such as cancer) in an individual. These may also be used for
 CC identifying substances capable of binding to or modulating the function
 CC of the polypeptide, capable of affecting the function of the
 CC corresponding gene, or capable of inhibiting the cell division cycle or
 CC cell cycle progression, preferably mitosis and/or meiosis. The present
 CC sequence represents an antagonist of cell cycle progression protein
 CC sequence.
 XX
 SQ Sequence 364 AA;

Query Match 70.1%; Score 1384; DB 8; Length 364;
 Best Local Similarity 70.3%; Pred. No. 1.8e-135;
 Matches 258; Conservative 51; Mismatches 54; Indels 4; Gaps 2;

QY 1 MYNNKRVFKKCAPNGKVTLYMGKRPVDVSGVEPIDGIVLVDDEYIRNKRFGQIVCS 60
 DB 1 MYNNKRVFKKCSPPNMNITLYMNRDPVDVSGVEPIDGIVLVDDEYIRNKRIFVQLVGN 60
 QY 61 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTLQERLLKLGSNAPFTFNIS 120
 DB 61 FRYGREDEDMIGLRPQKELTLVSQVCP-PQKODIQLTMQERLLKLGSNAPFTFMQMP 119
 QY 121 PNAPSSVTLQOGEDNDGDCGVSYVVKIFAGESETDRTHRSSTVTLGIRKIOFAPTKQG 180
 DB 120 PSSPASVVLQOKASDESQPCGVQYFVKIFGTGSDCDRSHRSSTINLGIRKVOYAPTKQGI 179
 QY 181 QGCTLVKRDPMSPGELSEVTLDKQLYHGERIGVNICIRNNSNMVKYKIKAMVOQGVND 240
 DB 180 QGCTVVRKDFLSPGELSEVTLDKQLYHGERIGVNICIRNNSNMVKYKIKAMVOQGVND 239
 QY 241 VVLFONGSYRNTVASLETSEGCPIOPGSSLOKVMYTLPLSSNKORRGIALDGOIKRQDO 300
 DB 240 VVLFONGGFRNTIATMETSEGCPLNPSSLOKVMYVPTLVANCDRAGIAVGDGIKRXDT 299

QY	301	CLASTTLLAQPDRDAFVITTSYAVKYLFLGALGELSALPPLVLMHPRGKAVITA	360
DB	300	ALASTTLLASDPDARDAFGIIVSYAVKYLFLGALGELCAELPPLIIMHPKSRKAOL---	356
QY	361	DSQADVE	367
DB	357	EAEESIE	363
RESULT 5			
ABR84484	ID	ABR84484	standard; protein; 398 AA.
XX	ABR84484;		
AC	15-JAN-2004	(first entry)	
DT	Mosquito olfaction molecule, arrestin 2.		
XX	Arrestin 2; mosquito; olfaction; insecticide; antimalarial.		
OS	Anopheles gambiae.		
XX	Key	Location/Qualifiers	
FT	Misc-difference	152	
XX	/note= "Encoded by AG"		
XX	MO2003076590-A2.		
PD	18-SEP-2003.		
XX	10-MAR-2003; 2003WO-US007174.		
PF	08-MAR-2002; 2002US-00094240.		
PR	(UYVA-) UNIV VANDERBILT.		
XX	Zwibel LJ;		
PI	WPI: 2003-722331/68.		
DR	N-PSDB; ACF79731.		
XX	New mosquito arrestin 1 and 2 genes and polypeptides, useful for		
PT	identifying mosquito olfaction molecule binding compounds which reduce		
PR	the ability of mosquitoes to locate sources of bloodmeal, e.g. humans.		
XX	Claim 16; Fig 12b; 101pp; English.		
PS			
XX			
CC	The present sequence is the protein sequence of arrestin 2, a novel		
CC	mosquito olfaction molecule. The invention provides 9 novel mosquito		
CC	polypeptides and the nucleic acids encoding them. These are arrestin 1		
CC	and 2 and odorant receptor molecules 1-7. The odorant receptors function		
CC	in a ligand-induced signal transduction pathway for the activation of		
CC	mosquito olfaction. Arrestin functions to inhibit the activated signal		
CC	transduction cascade. Thus, the odorant receptors act as an 'on' switch,		
CC	and arrestin as an 'off' switch for the odorant detection system of the		
CC	mosquito. Methods are provided for identifying compounds that interfere		
CC	with the operation of the mosquito olfactory system, particularly		
CC	compounds that modulate arrestin 2 activity. These are useful for the		
CC	control of bloodmeals, particularly by reducing their ability to locate		
CC	sources of bloodmeal		
XX			
SQ	Sequence 398 AA;		
Query Match	51.8%;	Score 1023;	DB 7; Length 398;
Best Local Similarity	52.3%;	Pred. No. 1,4e-97;	
Matches 204;	Conservative 65;	Mismatches 111;	Indels 10; Gaps 7
QY	1	MYVNFVFPKCA.PNGKVTLLYMGKDPFVHVGSEPIDGIVLLDDEYIRDRNKVFGQIVCS	60
DB	1	MYVAVKVFPKSKA.PNGKVTLLYTLKRFPIHDHYCDPIDSVIYLDDEYLR-GRKFGQLITR	59
QY	61	FYVGEEDFWMGLNFQKELCLASEQIYPRPEKSDKEQTKQERLLIKLGSNAIPFTFNIS	120

[illegible][illegible]

DR WPI: 2002-599706/64.
DR N-PSDB; ABS51567.
PT New complex of protein-protein interactions between a bait Shigella
PT flexneri polypeptide and a prey mammalian or human placenta polypeptide
PT for treating or preventing bacillary dysentery in a mammal or human.
XX
XX
PS Claim 7; Page 117-118; 162pp; English.
CC The invention relates to a complex of protein-protein interactions
CC between a Shigella flexneri polypeptide (e.g. ospB, ospI, ipaB, ipaC,
CC ipaH9.8, ospG and ospC) and a mammalian polypeptide defined in the
CC specification. The complexes are formed using the yeast two-hybrid
CC system. Also included are (1) a recombinant host cell expressing the
CC interactions between the Shigella flexneri polypeptide and a mammalian
CC polypeptide defined in the specification; (2) selecting a modulating
CC compound that inhibits or activates the protein-protein interactions; (3)
CC a modulating compound obtained from the method of (2); (4) a SID
CC (selected interacting domain) polypeptide or its fragment or variant
CC comprising the human polypeptides appearing as ABG70042-ABG70242; (5) a
CC SID polynucleotide or its fragment or variant comprising encoding the
CC above polypeptides a vector comprising (5); (6) a recombinant host cell
CC containing the vector; and (10) a mammalian polypeptide defined in the
CC flexneri polypeptide and a mammalian polypeptide defined in the
CC specification. A pharmaceutical composition comprising the compound,
CC polypeptide or polynucleotide is useful for treating or preventing
CC shigellosis (bacillary dysentery) in a human or mammal. The present
CC sequence represents a human prey protein isolated by the yeast two-hybrid
CC assay, forming a complex of the invention with a Shigella protein
XX
SQ Sequence 418 AA;
Query Match 45.6%; Score 900.5; DB 5; Length 418;
Best Local Similarity 46.8%; Pred. No. 1e-84;
Matches 178; Conservative 77; Mismatches 112; Indels 13; Gaps 5;
QY 6 KVFKKCAPNGKVTLYMGKRDVFDVHSGVEPIDGIVLDDXEYIRDNKRVFGQIVCSFRYGR 65
DB 7 RVFKKASPNKGLTYVYLGKRDVFDHIDLVDVGVVLDPEYLYKE-RRVYVTLTCAFRYGR 65
QY 66 EEDBEWGLNFQKELCLASSEQIYPRPEKSDKEQTKLOERLLKKGNSAIPPTFNISPNAPS 125
DB 66 EDIDLVLGLTFRKDLFVANVQSFPPAPEDKKPLTRLQERLLKKGNSAIPPTFNISPNAPS 125
QY 126 SVTLQOGEEDNGDPCGSGYVYVKIFAGESETDRTHRSSTVTLGIRKIQFAPRKQOQPCCTL 185
DB 126 SVTLQPEPEPTGKACGVDEYKAFCAENLEEKHKHNSVRLVIRKQYAPRREPQPTAE 185
QY 186 VRKDFMLSPGELELVTLDKQLYLHGERIGVNICIRNNSNMVKKIKAMVQGVVVLFQ 245
DB 186 TTQGFMLSDKRLHLEASLDKEIYYHGEPISVNVHVTNTKTKVKKIKISVQYADICLFN 245
QY 246 NGSYRNTVASLETSSEGCPIOPGSSLOKVMYLTPLLSNKKORGIADGQIKRQDCLAST 305
DB 246 TAOYKCPVAMEEADD--TVAPSSTFPCVYTLTFLPANNREKRGIALDGKIKHEDTNLASS 303
QY 306 TLLAOPQORDAFGVIISYAVKVLFL--GALGELSA-----ELPFVLMHPKPGTK--A 355
DB 304 TLLREGANREILGIIVSYKVKVLVSRGGLGLASSDVAVLELPFLTMHPKKEBPPHR 363
QY 356 KVIHADSOADVETFRQDTID 375
DB 364 EVPNERTFVDTNLTLEDTND 383
RESULT 12
ID ADO89786 standard; protein; 418 AA.
XX ADO89786;
XX
XX
DT 21-OCT-2004 (first entry)
XX

DE Antagonist of cell cycle progression polypeptide #108.
XX
XX
KM Cytostatic; cancer; cell division cycle; mitosis; meiosis;
KM cell cycle progression.
XX
XX
OS Homo sapiens.
XX
PN WO2004063362-A2.
XX
PD 29-JUL-2004.
XX
XX
PF 31-DEC-2003; 2003WO-GB005635.
XX
PR 10-JAN-2003; 2003US-0439123P.
PR 06-MAY-2003; 2003US-0468402P.
XX
XX
FA (CYCL-) CYCLACEL LTD.
XX
PI Glover D, Bell G, Frenz L, Midgley C;
XX
XX
DR WPI: 2004-544089/52.
DR N-PSDB; ADO89785.
XX
XX
PT New cell cycle progression genes and proteins for modulating cell cycle
PT progression in cells, for preventing, treating or diagnosing cell
PT proliferative diseases (e.g. cancer) or for identifying modulators of
PT mitosis or meiosis.
XX
XX
XX
PS Claim 2; SEQ ID NO 216; 461pp; English.
CC The present invention relates to a polynucleotide for preventing,
CC treating or diagnosing a disease in an individual. The composition or the
CC polypeptide, polynucleotide or RNA precursor, or antibody is useful for
CC diagnosing, preventing or treating diseases (e.g. cell proliferative
CC diseases such as cancer) in an individual. These may also be used for
CC identifying substances capable of binding to or modulating the function
CC of the polypeptide, capable of affecting the function of the
CC corresponding gene, or capable of inhibiting the cell division cycle or
CC cell cycle progression, preferably mitosis and/or meiosis. The present
CC sequence represents an antagonist of cell cycle progression protein
XX
SQ Sequence 418 AA;
Query Match 45.6%; Score 900.5; DB 8; Length 418;
Best Local Similarity 46.8%; Pred. No. 1e-84;
Matches 178; Conservative 77; Mismatches 112; Indels 13; Gaps 5;
QY 6 KVFKKCAPNGKVTLYMGKRDVFDVHSGVEPIDGIVLDDXEYIRDNKRVFGQIVCSFRYGR 65
DB 7 RVFKKASPNKGLTYVYLGKRDVFDHIDLVDVGVVLDPEYLYKE-RRVYVTLTCAFRYGR 65
QY 66 EEDBEWGLNFQKELCLASSEQIYPRPEKSDKEQTKLOERLLKKGNSAIPPTFNISPNAPS 125
DB 66 EDIDLVLGLTFRKDLFVANVQSFPPAPEDKKPLTRLQERLLKKGNSAIPPTFNISPNAPS 125
QY 126 SVTLQOGEEDNGDPCGSGYVYVKIFAGESETDRTHRSSTVTLGIRKIQFAPRKQOQPCCTL 185
DB 126 SVTLQPEPEPTGKACGVDEYKAFCAENLEEKHKHNSVRLVIRKQYAPRREPQPTAE 185
QY 186 VRKDFMLSPGELELVTLDKQLYLHGERIGVNICIRNNSNMVKKIKAMVQGVVVLFQ 245
DB 186 TTQGFMLSDKRLHLEASLDKEIYYHGEPISVNVHVTNTKTKVKKIKISVQYADICLFN 245
QY 246 NGSYRNTVASLETSSEGCPIOPGSSLOKVMYLTPLLSNKKORGIADGQIKRQDCLAST 305
DB 246 TAOYKCPVAMEEADD--TVAPSSTFPCVYTLTFLPANNREKRGIALDGKIKHEDTNLASS 303
QY 306 TLLAOPQORDAFGVIISYAVKVLFL--GALGELSA-----ELPFVLMHPKPGTK--A 355
DB 304 TLLREGANREILGIIVSYKVKVLVSRGGLGLASSDVAVLELPFLTMHPKKEBPPHR 363
QY 356 KVIHADSOADVETFRQDTID 375

Db 364 EVPENETPVTNLIELDTND 383

RESULT 13

ID AAG67779 standard; protein; 418 AA.

XX AAG67779;

XX 10-DEC-2001 (first entry)

XX Amino acid sequence of human beta-arrestin 1A.

XX Arrestin; phosphorylation-independent arrestin mutant;
 KW G protein-coupled receptor; GPCR; GPCR ligand; retinitis pigmentosa;
 KW stationary night blindness; colour blindness; nephrogenic DI;
 KW isolated glucocorticoid deficiency; hyperfunctioning thyroid adenoma;
 KW familial hypocalcaemic hypercalcaemia; hyperparathyroidism;
 KW neurological disorder.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region 155..184 /note="putative phosphorylation-recognition region"

XX WO200167106-A2.

XX 13-SEP-2001.

XX 05-MAR-2001; 2001WO-US007304.

XX 03-MAR-2000; 2000US-0186706P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Berstein G;

XX WPI; 2001-602637/68.

XX Identifying a G protein-coupled receptor ligand, useful for treating e.g.
 PT retinitis pigmentosa, color blindness or neurological disorders, uses
 PT phosphorylation-independent arrestin mutants particularly suited for in
 PT vitro screening assays.

XX PS Disclosure; Page 46; 47pp; English.

XX The present sequence represents an arrestin protein. The specification
 CC describes phosphorylation-independent arrestin mutants. These mutants are
 CC used in screening assays to identify ligands and/or modulators of G
 CC protein-coupled receptors (GPCRs). A method for identifying a GPCR ligand
 CC comprises contacting a composition comprising the GPCR and a
 CC constitutively active arrestin mutant with a test compound; and
 CC determining the ability of the test compound to modulate binding of
 CC arrestin mutant to the GPCR, where modulation of binding indicates that
 CC the test compound is a GPCR ligand. The method is used for identifying
 CC potential ligands and/or modulators of GPCRs, particularly modulators,
 CC for use as human therapeutics. Modulators of GPCR may be used for
 CC treating patients having e.g. retinitis pigmentosa, stationary night
 CC blindness, colour blindness, nephrogenic DI, isolated glucocorticoid
 CC deficiency, hyperfunctioning thyroid adenomas, familial hypocalcaemic
 CC hypercalcaemia, hyperparathyroidism and neurological disorders. The
 CC methods may be used for screening pluralities of test compounds (e.g. a
 CC small molecule library of compounds) or a composition containing a
 CC plurality of GPCRs. The methods may be used in screening assays for
 CC identification of natural and surrogate agonists of orphan GPCRs, and for
 CC identification of GPCR antagonists and/or agonists

XX Sequence 418 AA;

Query Match 45.5%; Score 897.5; DB 4; Length 418;
 Best Local Similarity 46.8%; Pred. No. 2.1e-84;

Matches 178; Conservative 76; Mismatches 113; Indels 13; Gaps 5;

QY 6 KVFKKCAPNGKVTLYMGKRPVDHVSQVPEPIDGIVLDDDEYIRNRRVFGQIVCSFRYGR 65
 Db 7 RVFKKASPNGKLTIVYLCKRDPVDHIDLVDVDGVVLDPPELKE-RRVYVLTCAFRYGR 65
 QY 66 EDEVMGILNFOKELCLASEQIYPRPEKSDKEQTKLQERLKLKGSNAIPFTFNISPNAPS 125
 Db 66 EDDVLGLITTRKDLFVNAVQSFPPAPEDKKPLRLQERLKLKGEHAYVPTFELIPRLPC 125
 QY 126 SVTLQGGEDNDGDPGVSYVYKIPAGESETRDTHRSSTVTLGIRKIQFAPTKQGOQPC 185
 Db 126 SVTLQGPEDTGKAGVDYEVKAFCAENLEBKIKRNSVRLVIRKVQYADERPPOPTAE 185
 QY 186 VRKQPMLSPEGLLEVLTKDOLYHGERIGVNICIRNNSKMKYKIKAMQGVVVLQ 245
 Db 186 TTRFOLMSDKRLHESLDEIKIYHGPISVNAVHTNNTKTVKIKISVQYADICLFN 245
 QY 246 NGSYRNTVVASLETSEGPCIOPGSLQKVMYLTPLLSNKKORGIALDGOIKRQDOCLAST 305
 Db 246 TAQYKCFVAMEADD--TVAPSSTFCKVYTLTPTLANNREKGLADGKLKHEDTNLASS 303
 QY 306 TLLAQPDQDAFGVIISYAVKVLFGALGELSA----ELPVLMPKPKCTK--A 355
 Db 304 TLLREGANREILGITVYSKVYKLVESRGILGDLASSDVAVELPFTLMHPKPEEBPHR 363
 QY 356 KYIHADSGADVETFRQDTID 375
 Db 364 EVPENETPVTNLIELDTND 383

RESULT 14

ABG13574 ID ABG13574 standard; protein; 369 AA.

XX AC ABG13574;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #13565.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HUSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS77761.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX Claim 20; SEQ ID NO 43933; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used

in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at http://www.wipo.int/pub/published_pct_sequences

Sequence 369 AA;

Query Match 45.1%; Score 890; DB 4; Length 369;
Best Local Similarity 48.6%; Pred. No. 1,1e-83;
Matches 171; Conservative 75; Mismatches 100; Indels 6; Gaps 4;

6 KVFKKCAPNGKVTLYMGKRDVHDVSGVEPIDGIVLDDEYIRDNKRVFGQIVCSFRYGR 65
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
7 RVFKKASPNKGLTYLGLKRDVHDVLDVDPDGVLDVPELKE-RKVYVTLCAFRYGR 65
66 EEDVWGMLNFOKELCLASEQIYPRPEKSDKEQTKLQERLLKKGNSNAIPFTFNISPAAPS 125
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
66 EDLVLGLTFRKDLFVANVQSFPPAPEDKKDLTRLOERLLKKEBHAHPFFFEIIPMLPC 125
126 SVTLQGEDNDGDCGVSYYVKIFAGSETRTRHRSVTTLGIRKIQAPFKQGOQPCCTL 185
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
126 SVTLQPEBDTGKACGVDEKAFCAENLEKIKRNSVGLVIRKVDVAPFRPPQPAE 185
186 VRKDFMLSPGELEVLTLKQLYLHGERIGVNICIRNNSNMVKIKIAMVQGVVVLFQ 245
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
186 TTRFPLMSDRSLHLSLDEKELIYHGERISVNVHTNTNTVEKIKISVQVADICLGN 245
246 NGSYRNTVASLETSCEGPIQPGSSLOKVMYTLPLISSNKKRRGIALDQIKRQDCLAST 305
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
246 TAOYKCCVVALEADD--TVAPSSTFCKVYTLTPFLANNREKRGALDQKLKHEBDTLASS 303
306 TLLAQPPORDAFGVIIISAVKVKLFLGALGELSASLPFLVMHPK--GTCA 355
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
304 TLLREGANRETLGITVSYKVKLVV-SRGGDVAVELPFTLMHPKQGRTPA 354

RESULT 15

AAG67785 standard; proteinn; 382 AA.

AAG67785;

10-DEC-2001 (first entry)

An exemplary phosphorylation-independent arrestin mutant.

Arrestin; phosphorylation-independent arrestin mutant;
G protein-coupled receptor; GPCR; ligand; retinitis pigmentosa;
stationary night blindness; colour blindness; nephrogenic DI;
isolated glucocorticoid deficiency; hyperfunctioning thyroid adenoma;
familial hypocalcaemic hypercalcaemia; hyperparathyroidism;
neurological disorder.

Undentified.

MO00167106-A2.

13-SEP-2001.

05-MAR-2001; 2001WO-US007304.

03-MAR-2000; 2000US-0186706P.
(MILL-) MILLENNIUM PHARM INC.
Berelein G;
WPI; 2001-602637/68.

Identifying a G protein-coupled receptor ligand, useful for treating e.g. retinitis pigmentosa, color blindness or neurological disorders, uses PT phosphorylation-independent arrestin mutants particularly suited for in vitro screening assays.

Disclosure; Page 47; 47pp; English.

The present sequence represents an exemplary phosphorylation-independent arrestin mutant. Such mutants are used in screening assays to identify CC ligands and/or modulators of G protein-coupled receptors (GPCRs). A CC method for identifying a GPCR ligand comprises contacting a composition CC comprising the GPCR and a constitutively active arrestin mutant with a CC test compound; and determining the ability of the test compound to CC modulate binding of arrestin mutant to the GPCR, where modulation of CC binding indicates that the test compound is a GPCR ligand. The method is CC used for identifying potential ligands and/or modulators of GPCRs, CC particularly modulators, for use as human therapeutics. Modulators of CC GPCR may be used for treating patients having e.g. retinitis pigmentosa, CC stationary night blindness, colour blindness, nephrogenic DI, isolated CC glucocorticoid deficiency, hyperfunctioning thyroid adenomas, familial CC hypocalcaemic hypercalcaemia, hyperparathyroidism and neurological CC disorders. The methods may be used for screening pluralities of test CC compounds (e.g. a small molecule library of compounds) or a composition CC containing a plurality of GPCRs. The methods may be used in screening CC assays for identification of GPCRs. The methods may be used in screening CC GPCRs, and for identification of GPCR antagonists and/or agonists

Sequence 382 AA;

Query Match 44.9%; Score 885; DB 4; Length 382;
Best Local Similarity 48.3%; Pred. No. 3.8e-83;
Matches 167; Conservative 77; Mismatches 98; Indels 4; Gaps 3;

6 KVFKKCAPNGKVTLYMGKRDVHDVSGVEPIDGIVLDDEYIRDNKRVFGQIVCSFRYGR 65
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
8 RVFKKSPNCKLTLYLGLKRDVHDVLDVDPDGVLDVPELMD-RKVYVTLCAFRYGR 66
66 EEDVWGMLNFOKELCLASEQIYPRPEKSDKEQTKLQERLLKKGNSNAIPFTFNISPAAPS 125
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
67 EDLVLGLTFRKDLFATYQAFPPVPPRPPRDLORLKRKGGONHPPFFFTIPOMLPC 126
126 SVTLQGEDNDGDCGVSYYVKIFAGSETRTRHRSVTTLGIRKIQAPFKQGOQPCCTL 185
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
127 SVTLQPEBDTGKACGVDFEIRAFCAKSLSEKHKNSVGLVIRKVDVAPFRPEKGPQPSAE 186
186 VRKDFMLSPGELEVLTLKQLYLHGERIGVNICIRNNSNMVKIKIAMVQGVVVLFQ 245
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
187 TTRFPLMSDRSLHLSLDEKELIYHGERISVNVHTNTNTVEKIKISVQVADICLFS 246
246 NGSYRNTVASLETSCEGPIQPGSSLOKVMYTLPLISSNKKRRGIALDQIKRQDCLAST 305
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
247 TAOYKCCVVALEADD--QVAPSSTFCKVYTLTPFLSSNREKRGALDQKLKHEBDTLASS 304
306 TLLAQPPORDAFGVIIISAVKVKLFLGALGELSASLPFLVMHPK 351
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
305 TIVKGANKEVLGITVSYKVKLVV-SRGGDVAVELPFLVMHPK 349

Search completed: May 20, 2006, 22:26:20
Job time : 198 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 20, 2006, 22:44:57 ; Search time 41 Seconds
(without alignments)
898.805 Million cell updates/sec

Title: US-10-056-405-2

Perfect score: 1973
Sequence: 1 MVYFKVFKKCAPNGKVTLY.....ADVETFRQDTTIDQASVDPE 363

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1499	76.0	381	2	B56607 arrestin homolog -
2	1384	70.1	364	2	A34867 arrestin - fruit f
3	1335	67.7	363	2	A55081 arrestin 1 - blueb
4	993.5	50.4	407	2	A56607 arrestin homolog -
5	977.5	49.5	401	2	S11566 arrestin homolog -
6	975.5	49.4	401	2	A34856 49k photoreceptor
7	942.5	47.8	401	2	B55081 arrestin 2 - blueb
8	935.5	45.8	418	2	A34851 beta-arrestin, bra
9	903.5	45.2	418	2	B43404 beta-arrestin 1, r
10	891.5	45.0	418	2	B46682 beta-arrestin 1, s
11	887	44.7	420	2	A47140 arrestin ar3L - b
12	882	44.1	409	2	S18984 arrestin - human (
13	871	44.1	407	2	S68253 arrestin isoform 1
14	869.5	44.1	410	2	A59279 beta-arrestin 2 -
15	865	43.8	454	2	T34297 hypothetical prote
16	863	43.7	415	2	S68255 arrestin isoform 1
17	861	43.6	405	2	S68254 arrestin isoform 2
18	810	41.1	387	2	S15104 cone arrestin - At
19	785.5	39.8	389	2	S68175 cone arrestin - bu
20	784.5	39.8	389	2	S68172 cone arrestin - no
21	783.5	39.7	403	2	JS0066 S-antigen - mouse
22	780.5	39.6	389	2	S38943 arrestin - human
23	775.5	39.3	403	2	S03960 S-antigen - rat
24	768.5	39.0	404	2	A28404 S-antigen - bovine
25	761	38.6	405	2	A30357 retinal S-antigen
26	731.5	37.1	396	2	S68173 rod arrestin - nor
27	731	37.1	387	2	S54423 arrestin-C - human
28	729.5	37.0	396	2	S68174 rod arrestin - bul
29	134	6.8	92	2	I70113 C-arrestin - rat (

30	129	6.5	378	2	T28112 hypothetical prote
31	118.5	6.0	427	2	T23954 hypothetical prote
32	111.5	5.7	354	2	T26507 hypothetical prote
33	111.5	5.7	471	2	T15155 hypothetical prote
34	111.5	5.7	2413	2	S34670 splicing factor PR
35	110.5	5.6	344	2	T33421 hypothetical prote
36	110	5.6	456	2	T29948 hypothetical prote
37	107.5	5.4	312	2	T20949 hypothetical prote
38	107.5	5.4	460	2	T23955 hypothetical prote
39	106.5	5.4	347	2	T33420 hypothetical prote
40	106	5.4	347	2	S31144 mkl protein - Myo
41	104	5.3	338	2	F87145 ABC transporter AT
42	102.5	5.2	464	2	T16826 hypothetical prote
43	101.5	5.1	1804	2	T34518 nestin - golden ha
44	100	5.1	359	2	B70534 probable ribonucle
45	99.5	5.0	600	2	S65788 Ku antigen 70K cha

ALIGNMENTS

RESULT 1

B56607
arrestin homolog - tobacco budworm
C:Species: Heliothis virescens (tobacco budworm)
C>Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
C:Accession: B56607
R:Raming, K.; Freltag, J.; Krieger, J.; Breer, H.
Cell. Signal. 5, 69-80, 1993
A:Title: Arrestin-subtypes in insect antennae.
A:Reference number: A56607; PMID:9319955; PMID:8452755
A:Accession: B56607
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar
A:Residues: 1-381 <RAM>
A:Molecule type: mRNA
A:Residues: 1-381 <RAM>
A:Cross-references: UNIPROT:P55274; UNIPARC:UPI0000126089
A:Experimental source: antennae
A:Note: sequence extracted from NCBI backbone (NCBI:P127926)
C:Superfamily: arrestin

Query Match	76.0%; Score 1499; DB 2; Length 381;
Best Local Similarity	72.7%; Pred. No. 1.2e-110;
Matches	277; Conservative 51; Mismatches 51; Indels 2; Gaps 2;
QY	1 MVYFKVFKKCAPNGKVTLYMGKRDVDAHSGVEPIIGIVLVDDEYIRDRKRVGQIVCS 60
DB	1 MVYFKVFKKCAPNGKVTLYMGKRDVDAHSGVEPIIGIVLVDDEYIRDRKRVGQIVCS 59
QY	61 FRVGRDEVMGINFQKELCLASFOIYRPRKSDKEQTKLOERLLKKGSAIPFTFNIS 120
DB	60 FRVGRDEVMGINFQKELCLASFOIYRPRKSDKEQTKLOERLLKKGSAIPFTFNIS 119
QY	121 PNASSVTLOQEDNDNPGCVSYVYKIFAGESETDRTHRSJVTLLGIRKIQFAPYKQ 180
DB	120 PNASSVTLOQEDNDNPGCVSYVYKIFAGESETDRTHRSJVTLLGIRKIQFAPYKQ 179
QY	181 QPCTLVKDFMLSGELFLEVTLDPKQYLNGERGAVNICIRNNSNKKVKKIKAVVQGV 240
DB	180 QPCTLVKDFMLSGELFLEVTLDPKQYLNGERGAVNICIRNNSNKKVKKIKAVVQGV 239
QY	241 VVLFQNGSYNTVSLFETSECPLOPSSLOKVVYLTPLLSNKKRGIALDQIKRQDQ 300
DB	240 VVLFQNGSYNTVSLFETSECPLOPSSLOKVVYLTPLLSNKKRGIALDQIKRQDQ 299
QY	301 CLASTTLLAOPDQDAFVILSYAVKVLFLGALGELSLAPFLVMHPKRGYAKVIHA 360
DB	300 TLASTTLLDPPDQDAFVILSYAVKVLFLGALGELSLAPFLVMHPKRGYAKVIHA 358
QY	361 DSQADVETFRQDTTIDQASVD 381
DB	359 DSQADVETFRQDTTIDQASVD 379

RESULT 2

A34867
arrestin - fruit fly (*Drosophila melanogaster*)
C/Species: *Drosophila melanogaster*
C/Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 09-Jul-2004
C/Accession: A34867; A34868
R/Smith, D.P.; Shieh, B.H.; Zuker, C.S.
Proc. Natl. Acad. Sci. U.S.A. 87, 1003-1007, 1990
A/Title: Isolation and structure of an arrestin gene from *Drosophila*.
A/Reference number: A34867; MUID:90138925; PMID:1689056
A/Accession: A34867
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-364 <SWI>
A/Cross-references: UNIPROT:P15372; UNIPARC:UPI000000069; GB:M30177
R/Hyde, D.R.; Mecklenburg, K.L.; Pollock, J.A.; Vitrelic, T.S.; Benzer, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 1008-1012, 1990
A/Title: Twenty *Drosophila* visual system cDNA clones: one is a homolog of human arrestin
A/Reference number: A34868; MUID:90138926; PMID:2105491
A/Accession: A34868
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-364 <HND>
A/Cross-references: UNIPARC:UPI000000069; GB:M30140; NID:9156961; PIDN:AAA28380.1; PID:
A/Gene: FlyBase:Ar1
A/Cross-references: FlyBase:Fbgn0000120
A/Intons: 36/3; 306/3; 349/3
C/Superfamily: arrestin

Query Match

Best Local Similarity 70.1%; Score 1384; DB 2; Length 364;
Matches 259; Conservative 51; Mismatches 54; Indels 4; Gaps 2;

QY 1 MVTNFKVFKKCAPNGKATLYMGKRDVVDHSGVEPIGIVLDEYIRDNKKYFGQIVCS 60
DB 1 MVTNFKVFKKCAPNGKATLYMGKRDVVDHSGVEPIGIVLDEYIRDNKKYFGQIVCS 60
QY 61 FRYGREDEWVGINFQKELCLASBOIYPRPEKSKQETKLOERLLKKGSMNAPFTFNIS 120
DB 61 FRYGREDEWVGINFQKELCLASBOIYPRPEKSKQETKLOERLLKKGSMNAPFTFNIS 120
QY 121 PNASSVTLOQGEDNDGPGCVSYVYKIFAGESETDTRHRSVTTLGIRKIQFAPTKQG 180
DB 120 PPSASVVLQKQKASDESQPGVQYFVKIFGDSQCDRSHRSTVNLGIRKQVAPTKQGI 179
QY 181 QPCTLVKDFMLSPGELLEVTLDKQLYHGERIGVNICIRNNSNKKVKKIKAMVQGV 240
DB 180 QPCTLVKDFMLSPGELLEVTLDKQLYHGERIGVNICIRNNSNKKVKKIKAMVQGV 239
QY 241 VVLFQNGSYRNTVASETSBGCPLOPGSSIQKMYLTPLLSSNKKORGIALLDQIKRQD 300
DB 240 VVLFQNGSYRNTVASETSBGCPLOPGSSIQKMYLTPLLSSNKKORGIALLDQIKRQD 299
QY 301 CLASTLLAOPDORDAFVGIISAVVKKLFLGALGELSLELPVLMHPRKTKAVIHA 360
DB 300 ALASTLLAOGDARDAGIIVSVAVKKLFLGALGELSLELPVLMHPRKTKAVIHA 356
QY 361 DSGADVE 367
DB 357 EAEGSIE 363

RESULT 3

A55081
arrestin 1 - bluebottle fly (*Calliphora vicina*)
C/Species: *Calliphora vicina*
C/Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C/Accession: A55081; S44291
R/Bangerter, A.; Mallick, D.; Whitney, M.; Paulsen, R.
J. Biol. Chem. 269, 26969-26975, 1994
A/Title: Mechanism of arrestin 2 function in rhodometric photoreceptors.
A/Reference number: A55081; MUID:95014564; PMID:7929436

A/Accession: A55081
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-363 <ELA>
A/Cross-references: UNIPROT:P51466; UNIPARC:UPI0000126075; GB:X79072; NID:9483527; PIDN:
A/Note: the source is designated as *Calliphora erythrocephala*
C/Superfamily: arrestin

Query Match

Best Local Similarity 67.7%; Score 1335; DB 2; Length 363;
Matches 248; Conservative 57; Mismatches 55; Indels 8; Gaps 2;

QY 1 MVTNFKVFKKCAPNGKATLYMGKRDVVDHSGVEPIGIVLDEYIRDNKKYFGQIVCS 60
DB 1 MVTNFKVFKKCAPNGKATLYMGKRDVVDHSGVEPIGIVLDEYIRDNKKYFGQIVCS 60
QY 61 FRYGREDEWVGINFQKELCLASBOIYPRPEKSKQETKLOERLLKKGSMNAPFTFNIS 120
DB 61 FRYGREDEWVGINFQKELCLASBOIYPRPEKSKQETKLOERLLKKGSMNAPFTFNIS 119
QY 121 PNASSVTLOQGEDNDGPGCVSYVYKIFAGESETDTRHRSVTTLGIRKIQFAPTKQG 180
DB 120 PPSASVVLQKQKASDESQPGVQYFVKIFGDSQCDRSHRSTVNLGIRKQVAPTKQGI 179
QY 181 QPCTLVKDFMLSPGELLEVTLDKQLYHGERIGVNICIRNNSNKKVKKIKAMVQGV 240
DB 180 QPCTLVKDFMLSPGELLEVTLDKQLYHGERIGVNICIRNNSNKKVKKIKAMVQGV 239
QY 241 VVLFQNGSYRNTVASETSBGCPLOPGSSIQKMYLTPLLSSNKKORGIALLDQIKRQD 300
DB 240 VVLFQNGSYRNTVASETSBGCPLOPGSSIQKMYLTPLLSSNKKORGIALLDQIKRQD 299
QY 301 CLASTLLAOPDORDAFVGIISAVVKKLFLGALGELSLELPVLMHPRKTKAVIHA 360
DB 300 SLASTLLAOGDARDAGIIVSVAVKKLFLGALGELSLELPVLMHPRKTKAVIHA 354
QY 361 DSGADVE 368
DB 355 --QPEAT 360

RESULT 4

A56607
arrestin homolog - migratory locust
C/Species: *Locusta migratoria* (migratory locust)
C/Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
C/Accession: A56607
R/Raming, K.; Freitag, J.; Krieger, J.; Breer, H.
Cell. Signal. 5, 69-80, 1993
A/Title: Arrestin-subtypes in insect antennae.
A/Reference number: A56607; MUID:93199955; PMID:8452755
A/Contents: antennae
A/Accession: A56607
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-407 <RAM>
A/Cross-references: UNIPROT:P32122; UNIPARC:UPI0000126088; GB:S57174; NID:9298755; PIDN:
A/Note: sequence extracted from NCBI backbone (NCBIN:127923, NCBI:P.127925)
C/Superfamily: arrestin

Query Match 50.4%; Score 993.5; DB 2; Length 407;
Best Local Similarity 52.1%; Pred. No. 1e-70;
Matches 202; Conservative 64; Mismatches 107; Indels 15; Gaps 8;

QY 6 KVFKKCAPNGKATLYMGKRDVVDHSGVEPIGIVLDEYIRDNKKYFGQIVCSFRYGR 65
DB 14 KVFKKTPNGKATLYMGKRDVVDHSGVEPIGIVLDEYIRDNKKYFGQIVCSFRYGR 72
QY 66 EEDWVGINFQKELCLASBOIYPRPEKSKQETKLOERLLKKGSMNAPFTFNISNAPS 125
DB 73 EEDWVGINFQKELCLASBOIYPRPEKSKQETKLOERLLKKGSMNAPFTFNISNAPS 131
QY 126 SVTLQOGEDNDGPGCVSYVYKIFAGESETDTRHRSVTTLGIRKIQFAPTKQGO-PCT 184

Db 132 SVTLIQPEDDDGGKRLGWEYSVKTWGQHAEBKHKRSVTLAIKKLDYAPFTRGRRLPSS 191

Qy 185 LYRKDFMLSPBELEVTYLDKQYLNGERIGVNI CIRNNSHKATKXIKAMVQGVVDVLF 244

Db 192 LVSGFGFTFSQKINLEVTLDREIYHGEKLANAYINNNSKTKVNIKVYVQGVCEVTMV 251

Qy 245 QNGSYRNTVASLETSBEGCPIDPGSSLOKRWMLTPLSSNKKORGIATLDGQIKRDQCLAS 304

Db 252 -NAOFSRHVALETRREGCPITPGASFTTKVFLVWCAASNKORYGIATLDGYLKDDVNLAS 310

Qy 305 TTLLAQ- PDQSDAFGVITSYAVKYLFLGALGEGSELPEVLNHPKPGT-----KAKYIH 359

Db 311 STVSEGNCTTDAIGIVISTSLRYKXNLGCGELQDVPFPKLHPAGTNEREKAQAI- 369

Qy 360 ADSQADVEYTRQD-----TIDQASVDPE 383

Db 370 -KKKMSLETRRYENSCTAADDNDNIVEE 396

QY	DB	Query March	Best Local Similarity	Score	977.5;	DB 2;	Length	401;
				48.5%;	Pred. No. 1.9e-69;			
				Matches 190;	Conservative 76;	Mismatches 113;	Indels 13;	Gaps 6;
QY	1	MYNFKYFKKCAPNGKVTLYMGKRDVVDHVGVEPIDIVLDELDEYIRDNKRVFGQIVCS	60					
DB	1	MVSVKVFVKKATPNCKVTFYLGRRDFIDHLDVCPVDGVIVPEPEYLR-NRKVFQQLATT	59					
QY	61	FRYGRDEEVNGLNFQKELCLASEDQIYPRPEKSDKEQTKLOERLLKLGSAIPTFNIS	120					
DB	60	YRYGGEDEVNMGVSKSLILSRDEIVPM-TNPNNEMTPMOEKLVRKKGSAHPETFAFP	118					
QY	121	PNAPSSTVLOOGEEDNDGPPCGSVYVVKIFAGESEETDRHRSSTVLYGIRKIQAPFTKQGO	180					
DB	119	PNSPSSTVLOOGEEDNGKPLGVETIIRAFVGDSEDDRGHKSSMSVLYKIQYAPLNGQ	178					
QY	181	Q-PCTLVKRDPMFLSGEDELVEVTLDKQLYLHGERIGVNICIRNNSNKKVKKIKANVQGV	239					
DB	179	RLPSLTVKSGFTFSSNGKISLEVTLLDREIYYHGEKTAATQVSNNSKKSVKSIKPIVQHT	238					
QY	240	DVFLFQNSYRNTVASLSTSECCPFIQPGSSLOKQWYTLPLSSNQGRGIALDQIKOD	299					
DB	239	EITWV-NAQFSKRVAAQLETKEGCPITPGANTLTKTYLLPLLAANNDRHGIALDGLKQED	297					
QY	300	QCLASTTLLAQ-PDQRDAFGVLIISAIVKVLFLGALGELSALPFLVMHPKPGT-----	353					
DB	298	VNLASTVWQEGKATGDAQGIIVISYVRHKLKNCGLTGEMQMDVPFLKLOPAPGTIEKKR	357					
QY	354	--KAKVTIHAQSDAVETFRPDITIQQAQSVDF	382					
DB	358	SNAMKKMSIEQHRNVKGGYYQDDDNIVFEDF	389					

RESULT 6
A34856
49k photoreceptor protein - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 09-Jul-2004
C:Accession: A34856
R:Yamada, T.; Takahashi, Y.; Komori, N.; Kobayashi, H.; Sakai, Y.; Hotta, Y.; Matsumoto, I.
Science 248, 483-485, 1990
A:Title: A 49-kilodalton phosphoprotein in the *Drosophila* photoreceptor is an arrestin homologue
A:Reference number: A34856; MUID:30232360; PMID:2158671
A:Accession: A34856
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-401 <YAMA>
A:Cross-references: UNIPROT: P19107; UNIPARC:UPI0000126081; GB:M32141; NID:g158157; PIDN:
C:Genetics:
A:Gene: FlyBase:Arr2
A:Cross-references: FlyBase:FBgn0000121
C:Superfamily: arrestin

Query Match 49.4%; Score 975.5; DB 2; Length 401;
Best Local Similarity 48.5%; Pred. No. 2,7e-69;
Matches 190; Conservative 74; Mismatches 115; Indels 13; Gaps 6;

```
Oy      1 MYNFKVKKCAPNGKVTLYMKRDFVDHVSQVEPIDGIYVLDDERYIDRNKRVCQIYCS   60  
Db      1 MVASVKVFKKATPNGKVTFYLGRDPIDHIDYDPDVGVIVBEDYLK-NRKVRQLATT    59  
Oy      61 PNYGEEDWVGILNFCKECLIASEQIYPREKSDKEOTKLQERLLTKLSNAIPPTFNIS   120  
Db      60 YRYGEBDEDMWGKRSKSELILCREQIVPM-TINEMEMTPMQEKLVRLKSANHPHTFHP   118  
Oy     121 PNAPSVTILOQEEDNDGDPCGSYYVIKFASESETDRTHRRSTVTLGIRKIQAFTKCGQ   180  
Db     119 PMSPSVTVLOQEGDDDGKGFLGVETEYTRAFVGEDSEDDRQHRSWSVLIYKIQVAPLNRGQ  178  
Oy     181 Q-PCTLVRDPMLSPELELTLDKQLYIHGERIGNICLRNNSNMVKIKAMVOGCY       239  
Db     179 RLPSSLVSGTFFSNKSLILEVTLDBREITYHGELTAATAVOVSNSKSVSKICKITVHT   238  
Oy     240 DVLVLONGSYRTYVASLETSEGPCIOGSAJLQCKMYTTPLLSNSKNORGLALDQIKRD   299  
Db     239 EITMV-NAQFSKHVALDEFKEGCPITPGNALTTFTFYILIPLAANKKDRIHALDGHXOD   297  
Oy     300 OCIAASTLLAQ-PDQRDAFGVIISYAVKVLPLGALCGEISAELPFVLMEHKPQT-----  353  
Db     298 VMLASTIMVQEGKSTDACGIVISYSVRIRKINGCCTLGGEMOTDVPFKLLQAPGTIEKKR   357  
Oy     354 ---KAKVHADSOADVETPRODTIIDQASIVDF 382  
Db     358 SNAMKKKKSIEQHRNVKGYIDDNDNIVERBDF 389
```

RESULT 7

B55081
arrestin 2 - bluebottle fly (*Calliphora vicina*)
C/Species: Calliphora vicina
C/Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C/Accession: B55081, S44292
R/plangerger, A.; Mallick, D.; Whitney, M.; Paulsen, R.
J Biol Chem. 269, 26969-26975, 1994
A>Title: Mechanism of arrestin 2 function in rhodometric photocoreceptors.
A/Reference number: A55081, PMID:95014564; PMID:7929436
A/accession: B55081
A/status: preliminary
A/molecule type: mRNA
A/residues: 1-401 <PI>
A/Cross-references: UNIPROT:P51487; UNIPARC:UPI000016B8DC; EMBL:X79073; NID:G483583; PID:A>Note: the source is designated as Calliphora erythrocephala
C/superfamily: arrestin

Query Match 47.8%; Score 942.5; DB 2; Length 401;

```

Best Local Similarity 47.7%; Pred. No. 1,1e-66;
Matches 187; Conservative 70; Mismatches 122; Indels 13; Gaps 6;

QY      1 M V Y N F K Y F K K C A P N G K Y T L Y M G K R D F V D H V G E V P I G I V L D E Y I R D N R K Y G A I V C 60
Db      1 M V S V K P F K K A T P N G K T F Y I G R R H F I D H P Y I P D V G I V V D D Y L K - N R K F A Q L A T I 59

QY      61 F R Y G R E D E V M G L N F O K E L C L A S E Q I Y P R P E K S D K E O T K L Q E R L L K K L G S N A I P F T E N I S 120
Db      60 Y R Y G R E D E V M G V K F S K E L I C R E Q I V P M - G S N S M E M P T Q E K L V R K L G S N A H P F T E H P 118

QY      121 P N A S S V T L O Q G E D N D N D P C G V S Y V K I F A G E S E T D R H R S T Y T L G I R K I Q P A P T Q G Q 180
Db      119 P N S P S S V T L Q O E G D D L G R P L G V E Y T I R A Y V A D S E D D R O H K R S M S V L I K K L Q V A P P T R G Q 178

QY      181 Q - P C T I V R K D M L S G E L E V E L T D K O Y L G E R I G V N I C I R N N S N M V K K K I K M W O G V 239
Db      179 R L P S S L V S K G T F P S N G K I S L E V T I D R E I Y H G G V A A T V Q I N N S K A A V K A I K I F T I Q H T 238

QY      240 D V I L F O N G S Y N T V A S L E T S E C P I O P G S S I Q K T M Y L T P L L S N K O R G I A L D Q I K R O D 299
Db      239 E I T W V - N A Q F S K H V A Q L E T T K E G C P I T P G A N S K I F Y L I P L A S N N K D H G I A L D D H L M E D 297

QY      300 Q C L A S T I L L A O - P O R D A F G V I I S Y A V K V L F L G A L G E L S A E L P F V L M H P K G T - - - - - 353
Db      298 V N L A S T M V Q G K S T G D A C G I V I S Y S V R I K L N C G T L G E I Q T D V P F K L L G A P A G S V E K R 357

QY      354 - - - K A K V I H A D S Q A D V E T F R O D T I D Q A S V P F 382
Db      358 S N A M K M K S I Q H R N T K G Y Q D D D D N I V E D F 389

```

RESULT 8

beta-arrestin, brain - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 13-Jul-1990 #sequence_revision 21-Oct-1992 #text_change 09-Jul-2004
C:Accession: A34851; JG2052
R:Loise, M.J.; Benovic, J.L.; Codina, J.; Caron, M.G.; Lefkowitz, R.J.
Science 248, 1547-1550, 1990
A:Title: Beta-arrestin, a protein that regulates beta-adrenergic receptor function.
A:Reference number: A34851; PMID:90296080; PMID:2165110
A:Accession: A34851
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-418 <LOH>
A:Cross-references: UNIPROT:P17870; UNIPARC:UPI0000042307; GB:M33601; NID:g162691; PIDN:
A:Experimental source: brain
R:Stierne-Marr, R.; Gurevich, V.V.; Goldsmith, P.; Bodine, R.C.; Sanders, C.; Donoso, L.A.
J. Biol. Chem. 268, 15640-15648, 1993
A:Title: Polypeptide variance of beta-arrestin and arrestin3.
A:Reference number: A47140; PMID:93340166; PMID:8340388
A:Accession: JG2052
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-15, 'C', '17-30, 'L', '32, 'K', '34-83, 'Y', '85-176, 'K', '178-206, 'L', '208-333, 342-418 <
A:Cross-references: UNIPARC:UPI0000178BC1
A:Experimental source: lung, spleen
C:Comment: This protein is an arrestin homolog which acts analogously to desensitize the
C:Superfamily: arrestin
F:1-333, 342-418/ Product: beta-arrestin, brain #status predicted <MAT>
F:1-333, 342-418/ Product: beta-arrestin, lung #status predicted <MA2>

```

Query Match      45.8%; Score 903.5; DB 2; Length 418;
Best Local Similarity 47.1%; Pred. No. 1.4e-63;
Matches 179; Conservative 76; Mismatches 112; Indels 13; Gaps 5;

QY      6 KYFKCANGKAVTLWGKRD FVDHVS GVEPIDGI VWLDD EYIRDRKRVGQIVCSFRGR 65
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      7 RVFKKASNGKLTIVLGKRD FVDHIDLVEPVDGVVLVPELUKE RRYVYVLTCAFRGR 65
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      66 EDEVMGNFOKEKLCLASEQIYPRPKSKDEQTKLQERLLKKGASNALPFTFNISPNAPS 125
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db	66	EDLDVLGLTRFKRDLEVANNQSPRPAPEDKKRLRLRLOERLLIKLGBAHYPTFELIRPLRBC	125
Qy	126	SVTLLOQGEDDNGDPCGVSTYYVKIFAGESETDRTHRSSTVTLGRKIQFATTKQGOQSTL	185
Db	126	SVTLLOQGEDDTCAGGVNDYEVAKFCANENLEEKHNKNSVALYVRKQYAEPRPQPTAE	185
Qy	186	VKIDFMLSGBELELEVTLDRKQYLHGERIGVNICIRNNSKQMYKKIKAMYOQGVVLLFQ	245
Db	166	TTROGLMSKPRHLHLSASLDKEIYHNGEPISTVNNVHNTNTTKVKKIKISVROYADICFN	245
Qy	246	NCSTYNTVASLSTSECCPIQPGSSLOKMYLTPRLSSNKORGLADGQIKRQDQCLAST	305
Db	246	TAQYCSVAMEAAD--TVAPSTFCKYVTLTPFLNANREKRLADGLKXHEVTNLAASS	303
Qy	306	TLLAOPDQDAEGVLIISYAVKVKLFL--GALGELS-----ELPFLVLMHPKPTK--A	355
Db	304	TLLRGARREILIGIIVSYKVKVLVVSRRGLGDLASSDVAVELPFLMHPKREEBRPHR	363
Qy	356	KVIHADSQADVETFPQDITD	375
Db	364	EVPEHEETPVDTNLIELDTND	383

RESULT 9

beta-arrestin1 rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: B43404
R:Atcramadadl, H.; Arriza, J.L.; Aoki, C.; Dawson, T.M.; Codina, J.; Kwatra, M.M.; Snyder, J. Biol. Chem. 267, 17882-17890, 1992
A:Title: Beta-arrestin2, a novel member of the arrestin/beta-arrestin gene family.
A:Reference number: A43404; MID:92388146; PMID:1517224
A:Accession: B43404
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-418 <ATT>
A:Cross-references: UNIPROT:P29066; UNIPARC:UP10000126079; GB:M91589; NID:g945985; PIDN.:J.A:Note: sequence extracted from NCBI backbone (NCBI:P:112791)
C:Superfamily: arrestin

Query Match	45.8%	Score 903.5	DB 2	Length 418
Best Local Similarity	46.8%	Pred. No. 1,4e-63		
Matches 178	Conservative 78	Mismatches 111	Indels 13	Gaps 5
Qy	6 KYFKCAPNGKATLYWKGKDFVDHVSQVEPIDGIWLDDEYIRDNKRVFGQIYCSFRYGR 65			
Db	7 RVFKKASPRGKLTIVLIGKRDVDVHIDLVPDVGVLVDPEYLKE-RVVYVTLTCAFRYGR 65			
Qy	66 EEDVWGLNFQKELCLASEQIYPRPEKSDKEQTKLOERLLKATGSMALPFTFNISPNAPS 125			
Db	66 EQLDVGLGTFRRKDLFVAVNQSPFPAPEDKKBLTRLRERLLKKGEGHVPFFTEELRPMLPC 125			
Qy	126 SVTLQOGEEDNNGPQCVSYVYKIFAGESETDRTHRSQTVLGIKIQIOPAPTKQOQPCCTL 185			
Db	126 SVTLQOGEEDDTGACQVDYEVKAFCAENLEEKHKHNSVAVLVIRKQVYAPBRPQPTAE 185			
Qy	186 VKDFMLSPGELEEVTLDKQVLYHGERIGVNICIRNNSNMVKKIKAVNQGVVVLEQ 245			
Db	186 TTRQFLMSDKPLHLIASLDKEIYYHGEPISSVNHVHTNTNKTQVKKIKISVQYADICLFN 245			
Qy	246 NSQYRNTVASLPISECCPIQPGSLQKMYLTPLLSNKKRRGIALDGOIKRQOQCLAST 305			
Db	246 TAQYKCPVAMEEDD--TVAPSSTFCKVYVTLTPLPLANNRKKRGIALDGKLHEDTNILASS 303			
Qy	306 TLLAQPDQDAFGVILISYAVKVLFL--GALGELSA----ELPVLMPHKPGTK--A 355			
Db	304 TLLREANNEILGIILSYKVKVLLVSRGSLDLASSDVAVELPFLTLMHPKREEPHR 363			
Qy	356 KVIHADSQADVETFERODTID 375			
Db	364 EVPESETPVDTNLIELDTND 383			

Db 67 EDDLVLGLSPKDLFIATYQAFPEVPNPPRPTRLQDRLLKLGQNAHPFFETIPQNLPC 126
 Qy 126 SVTLQGEDNDGPGCGVSYVVKIFAGESEDRTRHRSSTVTLGIRKIQFAPTKGQOQPC 185
 Db 127 SVTLQPEPDTGKACGVDFEIRAFCAKSLERKSKRNSVLRIRKQVFAPEKPEQPSAE 186
 Qy 186 VRKDFMLSPGELLEVTLDKQLYLHGERIGVNICIRNNSNMVKIKIRAMVOQGVVLFQ 245
 Db 187 TTHPFLMSDRSLHLEASLDKELYHGEPLNVNVHTNNSKTIVKIKIVSVRQVADICLFS 246
 Qy 246 NGSYRNTVASLETSEGCPIQPGSSLOKVMYTLPLSSNKQRRGIALDGOIKRQDOCLAS 305
 Db 247 TAOYKCPVAQLEQDD--QVSPSSFTFCVYITPLLSNREKRKDALDGLKHEDTNLASS 304
 Qy 306 TLLAQPDQRDAFGVIISYAVVKLFLGALGELSALPFLVMHPKP 351
 Db 305 TIVKEGANKKEVLGLIVSYRVKVLV--SRGDVSELPFLVMHPKP 349

RESULT 13
 S68253
 arrestin isoform 1S, erythrocyte - rainbow trout
 C/Species: Oncorhynchus mykiss (rainbow trout)
 C/Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C/Accession: S68253
 R/Jahns, R.; Borgese, F.; Lindenthal, S.; Straub, A.; Morais, R.; Fievet, B.
 Biochem. J. 316: 497-506, 1996
 A/Title: Trout red blood cell arrestin (TRCAR), a novel member of the arrestin family:
 A/Reference number: S68253; MUID:96257743; PMID:8667393
 A/Accession: S68253
 A/Status: preliminary; nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-407 <JAH>
 A/Cross-references: UNIPROT:P51466; UNIPARC:UPI0000126077; GB:U48410; NID:G1215723; PID:
 C/Superfamily: arrestin

Query Match 44.1%; Score 871; DB 2; Length 407;
 Best Local Similarity 44.3%; Pred. No. 4,9e-61;
 Matches 171; Conservative 82; Mismatches 121; Indels 12; Gaps 5;
 Qy 6 KVFKKCAPNGKVTLYMGKRDVFDHVSQVEPIDGIVLDDDEYIRDNKRVFGQIVCSFRYGR 65
 Db 8 RVFKSSPNCKVLYVIGKRDVFDHLDQVDPVGVILVDPEYLKD-RKVFYTLTCAFRYGR 66
 Qy 66 EEDRWGMLNFOKELCLASEQIYRPREKSDKEQTKLOERLLKLGSNAPIPTFNISPNAPS 125
 Db 67 EDDLVLGLSRKLDIYITFOAFPIAERKANSRLQERLLKLGQOAHFFFTIPQNLPC 126
 Qy 126 SVTLQGEDNDGPGCGVSYVVKIFAGESEDRTRHRSSTVTLGIRKIQFAPTKGQOQPC 185
 Db 127 SVTLQPEPDTGKACGVDFEIRAFCAKSLERKSKRNSVLRIRKQVFAPEKPEQPSAE 186
 Qy 186 VRKDFMLSPGELLEVTLDKQLYLHGERIGVNICIRNNSNMVKIKIRAMVOQGVVLFQ 245
 Db 187 TTHPFLMSDRSLHLEASLDKELYHGEPLNVNVHTNNSKTIVKIKIVSVRQVADICLFS 246
 Qy 246 NGSYRNTVASLETSEGCPIQPGSSLOKVMYTLPLSSNKQRRGIALDGOIKRQDOCLAS 305
 Db 247 TAOYKCPVAQLEAD--QVSSSTFCVYITPLLDKREKRGIALDGLKHEDTNLASS 304
 Qy 306 TLLAQPDQRDAFGVIISYAVVKLFLGALGELSALPFLVMHPKP--TKAKVITHAD 361
 Db 305 TIVKDVNKEVLGLIVSYRVKVLV--SRGDVSELPFLVMHPKPTELPSRQSAVDP 363
 Qy 362 SQADVERT---FRODTIDQASVPE 383
 Db 364 SDPEIDTNLLEFETNSFQDDDFVFE 389

RESULT 14
 A59279
 beta-arrestin 2 - rat
 C/Species: Rattus norvegicus (Norway rat)

C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
 C/Accession: A59279; A43404; I70112
 R/Attremadel, H.; Arriza, J.L.; Aoki, C.; Dawson, T.M.; Codina, J.; Kwatra, M.M.; Snyder, J.
 submitted to Genbank, August 1995
 A/Reference number: A59279
 A/Accession: A59279
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-410 <ATT>
 A/Cross-references: UNIPROT:P29067; UNIPARC:UPI000012607D; GB:M91590; NID:G949986; PIDN:
 A/Experimental source: strain Sprague-Dawley, stage adult; tissue type brain; tissue lib
 R/Attremadel, H.; Arriza, J.L.; Aoki, C.; Dawson, T.M.; Codina, J.; Kwatra, M.M.; Snyder, J.
 J. Biol. Chem. 267: 17882-17890, 1992
 A/Title: Beta-arrestin2, a novel member of the arrestin/beta-arrestin gene family.
 A/Reference number: A43404; MUID:92388146; PMID:1517224
 A/Accession: A43404
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-320, 'A', 322-325, 'A', 327-330, 'A', 332-410 <AT2>
 A/Cross-references: UNIPARC:UPI0000178BC5; GB:M91590; NID:G949986
 A/Note: sequence extracted from NCBI backbone (NCBI:112790)
 A/Note: the sequence is revised in Genbank entry RATABRRS2, release 113.0
 R/Craft, C.M.; Whitmore, D.H.; Wlechniak, A.F.
 J. Biol. Chem. 269: 4613-4619, 1994
 A/Title: Cone arrestin identified by targeting expression of a functional family.
 A/Reference number: I55423; MUID:94140898; PMID:8308033
 A/Accession: I70112
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 295-410 <CRA>
 A/Cross-references: UNIPARC:UPI0000170BD4; EMBL:U03627; NID:G458202; PID:AAA17551.1; PII
 C/Superfamily: arrestin

Query Match 44.1%; Score 869.5; DB 2; Length 410;
 Best Local Similarity 48.1%; Pred. No. 6,5e-61;
 Matches 167; Conservative 76; Mismatches 99; Indels 5; Gaps 4;
 Qy 6 KVFKKCAPNGKVTLYMGKRDVFDHVSQVEPIDGIVLDDDEYIRDNKRVFGQIVCSFRYGR 65
 Db 8 RVFKSSPNCKVLYVIGKRDVFDHLDQVDPVGVILVDPEYLKD-RKVFYTLTCAFRYGR 66
 Qy 66 EEDRWGMLNFOKELCLASEQIYRPREKSDKEQTKLOERLLKLGSNAPIPTFNISPNAPS 125
 Db 67 EDDLVLGLSPKDLFIATYQAFPEVPNPPRPTRLQDRLLKLGQNAHPFFETIPQNLPC 126
 Qy 126 SVTLQGEDNDGPGCGVSYVVKIFAGESEDRTRHRSSTVTLGIRKIQFAPTKGQOQPC 185
 Db 127 SVTLQPEPDTGKACGVDFEIRAFCAKSLERKSKRNSVLRIRKQVFAPEKPEQPSAE 186
 Qy 186 VRKDFMLSP-GELEVTLDKQLYLHGERIGVNICIRNNSNMVKIKIRAMVOQGVVLF 244
 Db 187 TTHPFLMSDRSLHLEASLDKELYHGEPLNVNVHTNNSKTIVKIKIVSVRQVADICLFS 246
 Qy 245 QNSYRNTVASLETSEGCPIQPGSSLOKVMYTLPLSSNKQRRGIALDGOIKRQDOCLAS 304
 Db 247 TAOYKCPVAQLEQDD--QVSPSSFTFCVYITPLLSNREKRKDALDGLKHEDTNLASS 304
 Qy 306 TLLAQPDQRDAFGVIISYAVVKLFLGALGELSALPFLVMHPKP 351
 Db 305 TIVKDVNKEVLGLIVSYRVKVLV--SRGDVSELPFLVMHPKPTELPSRQSAVDP 350

RESULT 15
 T34297
 hypothetical protein F53H8.2 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
 C/Accession: T34297
 R/Bradshaw, H.; Gattung, S.
 submitted to the EMBL Data Library, November 1995
 A/Description: The sequence of C. elegans cosmid F53H8.
 A/Reference number: Z21501
 A/Accession: T34297

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 20, 2006, 22:37:51 ; Search time 301 Seconds
(without alignments)
1177.013 Million cell updates/sec

Title: US-10-056-405-2

Perfect score: 1973
Sequence: 1 MYNFKVFKKCAPNGKVTLY.....ADVETFRQDTIIDQASVDFE 383

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprotc:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1973	100.0	383	2	Q7PMG5 ANOGA
2	1973	100.0	383	2	Q95NR3 ANOGA
3	1515	76.8	381	2	Q9B1G3 9NEOP
4	1499	76.0	381	1	ARRH HELVI
5	1384	70.1	364	1	ARRA DROME
6	1335	67.7	363	1	ARR1 CALVI
7	1254	63.6	245	2	Q6VFP0 ANOGA
8	1219	61.8	269	2	Q5TNW2 ANOGA
9	1036	52.5	431	2	Q7Q2V9 ANOGA
10	1023	51.8	398	2	Q7Q5Q8 ANOGA
11	1002	50.8	470	2	Q9V393 DROME
12	993.5	50.4	407	1	ARRH LOCMI
13	982.5	49.8	401	1	ARRB DROME
14	977.5	49.5	401	1	ARRB DROME
15	953	48.3	390	2	Q5B1J0 DROME
16	937.5	47.5	400	1	ARRB CALVI
17	931	47.2	400	1	ARRH LIMPO
18	931	47.2	419	2	Q6CBW6 HALRO
19	922.5	46.8	418	2	Q6MYB1 CIOIN
20	919	46.6	412	2	Q641D8 XENLA
21	912.5	46.2	410	2	Q4R562 MACFA
22	912.5	46.2	410	2	Q8BTJ5 MOUSE
23	904.5	45.8	418	2	ARRB1 MOUSE
24	904.5	45.8	418	2	Q3UH95 MOUSE
25	903.5	45.8	418	1	ARRB1 BOVIN
26	903.5	45.8	418	1	ARRB1 RAT
27	900.5	45.6	418	1	ARRB1 HUMAN
28	900.5	45.6	418	2	Q2PP20 HUMAN
29	893	45.3	408	2	Q7T2D2 BRARE
30	888.5	45.0	435	1	ARRB CAEEL
31	887	45.0	420	1	ARRB2 BOVIN

32	885	44.9	409	1	ARRB2 HUMAN	P32121 homo sapien
33	885	44.9	409	2	Q2PP19 HUMAN	Q2PP19 homo sapien
34	885	44.9	409	2	Q5RCR4 PONPY	Q5RCR4 pongo pygma
35	881.5	44.7	435	2	Q5WNA5 CAEBR	Q5WNA5 caenorhabdi
36	881.5	44.7	409	2	Q6ICT3 HUMAN	Q6ICT3 homo sapien
37	880.5	44.6	410	1	ARRB1 RABIT	Q95223 oryctolagus
38	880	44.6	408	2	Q6DFC4 XENLA	Q6DFC4 xenopus lae
39	878.5	44.5	406	2	Q6PRK2 BRARE	Q6PRK2 brachydanio
40	876	44.4	408	2	Q6PYR2 XENLA	Q6PYR2 xenopus lae
41	871	44.1	407	1	ARR1 ONCMT	P51466 oncothrychu
42	869.5	44.1	402	2	Q3TRC8 MOUSE	Q3TRC8 mus musculu
43	869.5	44.1	410	1	ARRB2 MOUSE	Q91Y14 mus musculu
44	869.5	44.1	410	1	ARRB2 RAT	P29067 rattus norv
45	869.5	44.1	410	2	Q5P2E0 MOUSE	Q5P2E0 m novel pro

ALIGNMENTS

```

RESULT 1
ID Q7PMG5 ANOGA PRELIMINARY; PRT; 383 AA.
AC Q7PMG5;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 07-DEC-2004, sequence version 2.
DT 07-FEB-2006, entry version 12.
DE ENSANGP0000012559.
GN ORFNames=ENSANG000000010080;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
OC Anophelinae; Anophelinae.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC
CC EMBL; AAB01008980; EAA1384.3; -; Genomic DNA.
CC GO; GO:0007600; P:sensory perception; IEA.
CC GO; GO:0007165; P:signal transduction; IEA.
CC InterPro; IPR000698; Arrestin.
CC InterPro; IPR011022; Arrestin.
CC InterPro; IPR011021; Arrestin_N.
CC PANTHER; PTHR11792; Arrestin_C; 1.
CC Pfam; PF02752; Arrestin_C; 1.
CC PRINTS; PR00309; Arrestin_N; 1.
CC ProDom; PD002099; Arrestin; 2.
CC PROSITE; PS00295; Arrestin; 1.
SQ SEQUENCE 383 AA; 42809 MW; FA9464385928B53B CRC64;
Query Match 100.0%; Score 1973; DB 2; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.1e-146;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYNFKVFKKCAPNGKVTLYGKRDPPDHVSGVPEPIGIVLDDERYLRDRKVGQIVCS 60
DB 1 MYNFKVFKKCAPNGKVTLYGKRDPPDHVSGVPEPIGIVLDDERYLRDRKVGQIVCS 60

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QY 61 FRVREDEWVGNLFQKELCLASEQIYPRPEKSDKEQTKQERLLKLGSNALPFTFNIS 120
DB 61 FRVREDEWVGNLFQKELCLASEQIYPRPEKSDKEQTKQERLLKLGSNALPFTFNIS 120
QY 121 PNAPSSVTLQOQEDNDPCGVSYVYKIPAGESETRTHRSSTVTLGIRKIQFAPTKQ 180
DB 121 PNAPSSVTLQOQEDNDPCGVSYVYKIPAGESETRTHRSSTVTLGIRKIQFAPTKQ 180
QY 181 QPCTLVKDFMLSPGSELEVTLDKQYLHGERIGVNICIRNNSNKKVKKIKAMVOQGV 240
DB 181 QPCTLVKDFMLSPGSELEVTLDKQYLHGERIGVNICIRNNSNKKVKKIKAMVOQGV 240
QY 241 VVLFQNGSYRNTVASLETSEGCPIQPGSLQKVMYLTPLSSNKKORRGIALDQIKRQ 300
DB 241 VVLFQNGSYRNTVASLETSEGCPIQPGSLQKVMYLTPLSSNKKORRGIALDQIKRQ 300
QY 301 CLASTTLLAOPDQDAFGVITISYAVKVLFLGALGSELAPVLMHPKGTAKAVIHA 360
DB 301 CLASTTLLAOPDQDAFGVITISYAVKVLFLGALGSELAPVLMHPKGTAKAVIHA 360
QY 361 DSQADVETFRDPTIDQASVDPE 383
DB 361 DSQADVETFRDPTIDQASVDPE 383

RESULT 2
095NF3 ANOGA
ID 095NF3 ANOGA PRELIMINARY; PRT; 383 AA.
AC 095NF3
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE Arrestin.
GN Name=Artr1;
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicidae; Anophelidae;
OC Anophelinae; Anopheles.
NCBI_TaxID=7165;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Antennae, and Head;
RX MEDLINE=21680430; PubMed=11822731; DOI=10.1007/s00436-002-0637-0;
RA Ricci I., Santolamazza F., Costantini C., Favia G.;
RT "Molecular characterization and chromosomal mapping of transcripts
RT having tissue-specific expression in the malaria mosquito anopheles
RT gambiae: possible involvement in visual or olfactory processes.";
RL Parasitol. Res. 88:1-8(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G3;
RX MEDLINE=21819361; PubMed=11792843; DOI=10.1073/pnas.022505499;
RA Merrill C.E., Riesgo-Escovar J., Pites R.J., Kafatos F.C.,
RA Carlson U.R., Zwebel L.J.;
RT "Visual arrestins in olfactory pathways of Drosophila and the malaria
RT vector mosquito Anopheles gambiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:1633-1638(2002).
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CC
CC EMBL; AJ304409; CAC39103.2; -; mRNA.
DR EMBL; AY017417; AAC54081.1; -; mRNA.
DR HSSP; P17870; 1G4M.
DR Ensembl; ENSANGG00000010080; Anopheles gambiae.
DR GO; GO:0007600; P:sensory perception; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000698; Arrestin.
DR InterPro; IPR011022; Arrestin_C.
DR InterPro; IPR011021; Arrestin_N.
DR PANTHER; PTHR11792; Arrestin; 1.
DR Pfam; PF02752; Arrestin_C; 1.
DR Pfam; PF00339; Arrestin_N; 1.

DR PRINTS; PR00309; ARRESTIN.
DR PROSITE; PS00295; ARRESTINS; 1.
SQ SEQUENCE 383 AA; 42809 MW; FA946438592B853E CRC64;
Query Match 100.0%; Score 1973; DB 2; Length 383;
Best Local Similarity 100.0%; Pred. No. 1,1e-146;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYVNFKFKKCAPNGKVTLMGKRDFFVDHSGVPEPIDGIIVLDDDEYIRDNRRKFGQIVCS 60
DB 1 MYVNFKFKKCAPNGKVTLMGKRDFFVDHSGVPEPIDGIIVLDDDEYIRDNRRKFGQIVCS 60
QY 61 FRVREDEWVGNLFQKELCLASEQIYPRPEKSDKEQTKQERLLKLGSNALPFTFNIS 120
DB 61 FRVREDEWVGNLFQKELCLASEQIYPRPEKSDKEQTKQERLLKLGSNALPFTFNIS 120
QY 121 PNAPSSVTLQOQEDNDPCGVSYVYKIPAGESETRTHRSSTVTLGIRKIQFAPTKQ 180
DB 121 PNAPSSVTLQOQEDNDPCGVSYVYKIPAGESETRTHRSSTVTLGIRKIQFAPTKQ 180
QY 181 QPCTLVKDFMLSPGSELEVTLDKQYLHGERIGVNICIRNNSNKKVKKIKAMVOQGV 240
DB 181 QPCTLVKDFMLSPGSELEVTLDKQYLHGERIGVNICIRNNSNKKVKKIKAMVOQGV 240
QY 241 VVLFQNGSYRNTVASLETSEGCPIQPGSLQKVMYLTPLSSNKKORRGIALDQIKRQ 300
DB 241 VVLFQNGSYRNTVASLETSEGCPIQPGSLQKVMYLTPLSSNKKORRGIALDQIKRQ 300
QY 301 CLASTTLLAOPDQDAFGVITISYAVKVLFLGALGSELAPVLMHPKGTAKAVIHA 360
DB 301 CLASTTLLAOPDQDAFGVITISYAVKVLFLGALGSELAPVLMHPKGTAKAVIHA 360
QY 361 DSQADVETFRDPTIDQASVDPE 383
DB 361 DSQADVETFRDPTIDQASVDPE 383

RESULT 3
09BIC9_9NEOP
ID 09BIC9_9NEOP PRELIMINARY; PRT; 381 AA.
AC 09BIC9
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE Arrestin.
GN Name=Artr1;
OS Acalaphus macaronius.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Neuroptera; Acalaphidae; Acalaphus.
NCBI_TaxID=146496;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=21184354; PubMed=11287006; DOI=10.1016/S0014-5793(01)02287-6;
RA Bentrop J., Schillo M., Gerdon G., Draelar G., Paulsen R.;
RT "UV-light-dependent binding of a visual arrestin 1 isoform to
RT photoreceptor membranes in a neuropteran (Acalaphus) compound eye.";
RL FEBS Lett. 493:112-116(2001).
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CC
CC EMBL; AJ303080; CAC36938.1; -; mRNA.
DR HSSP; P17870; 1G4M.
DR GO; GO:0007600; P:sensory perception; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000698; Arrestin.
DR InterPro; IPR011022; Arrestin_C.
DR InterPro; IPR011021; Arrestin_N.
DR PANTHER; PTHR11792; Arrestin; 1.
DR Pfam; PF02752; Arrestin_C; 1.
DR Pfam; PF00339; Arrestin_N; 1.
DR PRINTS; PR00309; ARRESTIN.

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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DR	PROSITE, PS00295; ARRESTINS; 1.	451DEF465969857D	CRC64:
SQ	SEQUENCE	381 AA; 42789 MW; 1.	
	Query Match	76.8%; Score 1515; DB 2; Length 381;	
	Best Local Similarity	75.7%; Pred. No. 1.3e-110;	
	Matches	289; Conservative 46; Mismatches 41; Indels 6; Gaps 4.	
QY	1	MVYNFKVKCAPNGKVTLLNGKRDVFDVHSGVEPIDGIIVLDEYI-RDNKRVFGIYC	59
DB	1	MVAANFKVKKSSPNKIKITITVLGKDPFVHSGVEPVDGLLDDDDYINQKERKVFQIYC	60
QY	60	SPRVREDEWVGNLFOKEICLASGOIYPRPKSKDEQTKOERLLKKLGSAIPEFTNI	119
DB	61	SFRVREDEWVGNLFRKDLTVLSQIYPSNKK--VETTKQDRLLIKLGPVALPFFKVL	118
QY	120	SPNASSVTLLQOGEDNDGDPGCVSYVYVXIFAESETDRTHRSSTYTLGIRKIQFAPTRQG	179
DB	119	PPNAPATITTLQGAADQGPQCVQVFLKAFVESDTERPHANASSVMOIRKQIYAPSRQG	178
QY	180	QQPCTLVKDFMLSPGELELEVTLDKQLYLHGERIGVNI CIRNNSNKKVYKIKAVYQGV	239
DB	179	RQPTVVRKDFMLSPGDELEVTLDKQLYHGEKIAVNI CIRNNSNKKVYKIKAMIQGV	238
QY	240	DVVLFGNSYRTVVASLETSEGCPIQPGSSLQKNWYLPPLSSNQRGIALDQIKRQD	299
DB	239	DVVLFGNQCYRTTIAHLETFEGCPIQPGSALQKNWYLPPLSSNQRDRRIADQIKRQD	298
QY	300	QCLASTTLLAOPDQDAFAVVISYVAVKYVLFALGAGELSAELPFVLMHPKPGTRAKVH	359
DB	299	TMLASTTLLANEGQDAFGLIYSYAVKYVLYGALGELALADPLFLMHPR-ENKRFH	357
QY	360	ADSOADVETFRQDTIDQOASVD	381
DB	358	ADSOADVEMFRQDTVD--PSVD	377
RESULT 4			
ARRH	HELV1	STANDARD;	PRT; 381 AA.
ID	ARRH HELV1		
AC	P55274;		
DT	01-OCT-1996, integrated into UniProtKB/Swiss-Prot.		
DT	01-OCT-1996, sequence version 1.		
DT	07-FEB-2006, entry version 26.		
DE	Arrestin homolog.		
OS	Heliothis virescens (Noctuid moth) (Owllet moth).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;		
OC	Noctuidae; Heliothinae; Heliothis.		
NC	NCBI Taxid=7102;		
RP	[1]		
RN	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Antenna.		
RX	MEDLINE=93199955; PubMed=8452755; DOI=10.1016/0898-6568(93)90009-B;		
RA	Ramwig K., Frettag J., Krieger J., Breier H.;		
RT	"Arrestin-subtypes in insect antennae.";		
RL	Cell. Signal. 5:69-80(1993).		
CC	-i- SIMILARITY: Belongs to the arrestin family.		
CC			
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CC	Distributed under the Creative Commons Attribution-NoDerivs License		
CC			
DR	PIR; B56607; B56607.		
DR	HSSP; P18770; 1G4M.		
DR	InterPro; IPR000698; Arrestin.		
DR	InterPro; IPR011022; Arrestin_C.		
DR	InterPro; IPR011021; Arrestin_N.		
DR	PANTHER; PTHR11792; Arrestin_1.		
DR	Pfam; PF02752; Arrestin_C_1.		
DR	Pfam; PF00339; Arrestin_N_1.		
DR	PRINTS; PR00309; ARRESTIN.		
DR	ProDom; PD002099; Arrestin_2.		
DR	PROSITE; PS00295; ARRESTINS; 1.		
KW	Sensory transduction.		

[illegible]

Db 300 ALASTTLIASQDARDAGIIVSYAVKVKLFLGALGSELCAELPFILMHKPKSRKAQI--- 356

Qy 361 DSQADVE 367
::: |
Db 357 EAEGSIE 363

RESULT 6

AR1 CALVI STANDARD; PRT; 363 AA.

ID AR1 CALVI
AC P51486;
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-1996, entry version 1.
DT 07-FEB-2006, entry version 28.
DE Phosrestin-2 (Phosrestin II) (Arrestin A) (Arrestin-1).
GN Name=AR1;
OS Calliphora vicina (Blue blowfly) (Calliphora erythrocephala).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygora;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=7373;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Retina;
RA MEDLINE=95014564; PubMed=7929436;
RX Planger A., Mallick D., Whitney M., Paulsen R.;
RT "Mechanism of arrestin 2 function in rhabdomeric photoreceptors."
RL J. Biol. Chem. 269:26969-26975 (1994).
CC -1- SIMILARITY: Belongs to the arrestin family.
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DR EMBL: X79072; CAAS5672.1; -; mRNA.
DR PIR: A55081; A55081.
DR HSSP: P17870; IG4M.
DR InterPro: IPR000698; Arrestin.
DR InterPro: IPR011022; Arrestin_C.
DR InterPro: IPR011021; Arrestin_N.
DR PANTHER: PTHR11792; Arrestin; 1.
DR Pfam: PF02752; Arrestin_C; 1.
DR Pfam: PF00339; Arrestin_N; 1.
DR PRINTS: PR00309; ARRESTIN.
DR ProDom: PD002099; Arrestin; 2.
DR PROSITE: PS00295; ARRESTINS; 1.
KW Sensory transduction; Vision.
FT CHAIN 1 363 /FTID=PRO_0000205214.
FT SQ SEQUENCE 363 AA; 40680 MW; 7C345D81BE46C23E CRC64;

Query Match 67.7%; Score 1335; DB 1; Length 363;
Best Local Similarity 67.4%; Pred. No. 1.8e-96;
Matches 248; Conservative 57; Mismatches 55; Indels 8; Gaps 2;

Qy 1 MYNFKVKKCAKPNKVTLYMGKRPVDHVSQVEPIQIVLDDYIRDNKRVQOIVCS 60
Db 1 MYVNFKIKFKKASPNMVTLYMNRREFVDSVTOVEBVDGIVLDDYIRDNKRI FQQLCN 60
Qy 61 FRYGSEEDVWGLNFOKEICLASSEIYPRPEKSDKBOFLQORLLKKUGSNAPPTFNIS 120
Db 61 FRYGSEEDVWGLNFOKEICLASSEIYPRPEKSDKBOFLQORLLKKUGSNAPPTFNIS 119
Qy 121 PNASPSVTLLQGGEDNDGDCGVSYYVKIFAGESETDRTTRRSTVTLGIRKIQFAPTKOQ 180
Db 120 PNASPSVTLLQGGEDNDGDCGVSYYVKIFAGESETDRTTRRSTVTLGIRKIQFAPTKOQ 179
Qy 181 QPCTLVKRDPMLSPEGLIEVTLDKQLYHGERIGVNICIRNNSNMVKKIRAMVOGQVD 240
Db 180 QPCTLVKRDPMLSPEGLIEVTLDKQLYHGERIGVNICIRNNSNMVKKIRAMVOGQVD 239
Qy 241 VVLFONGSYRNTVASIETSEGCPIQSGSLQKVMYLTPLLSNKKRGIALDGOIKRQDQ 300
Db 240 VVLFONGSYRNTVASIETSEGCPIQSGSLQKVMYLTPLLSNKKRGIALDGOIKRQDQ 299

Qy 301 CLASTTLAQDPORDARGIIVSYAVKVKLFLGALGSELCAELPFILMHKPKRGTAKVIA 360
Db 300 SLASTTLIAEQARDAGIIVSYAVKVKLFLGALGSELCAELPFILMHKPKSLKA----- 354

Qy 361 DSQADVET 368
|:: |
Db 355 --QPEAVT 360

RESULT 7

Q6VPP0 ANOQA PRELIMINARY; PRT; 245 AA.

ID Q6VPP0 ANOQA
AC Q6VPP0;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Arrestin (Fragment).
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygora;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=7165;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=4ARR, Yaounde, and L3-5;
RA Morlaix I., Foncon N., Simard F., Conhet A., Fontenille D.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
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DR EMBL: AY333991; AAR01116.1; -; Genomic DNA.
DR EMBL: AY333992; AAR01117.1; -; Genomic DNA.
DR EMBL: AY333993; AAR01118.1; -; Genomic DNA.
DR EMBL: AY333995; AAR01120.1; -; Genomic DNA.
DR EMBL: AY333996; AAR01121.1; -; Genomic DNA.
DR EMBL: AY333994; AAR01119.1; -; Genomic DNA.
DR HSSP: P08168; IAYR.
DR GO: GO:0007600; P: sensory perception; IEA.
DR GO: GO:0007165; P: signal transduction; IEA.
DR InterPro: IPR000698; Arrestin.
DR InterPro: IPR011022; Arrestin_C.
DR PANTHER: PTHR11792; Arrestin; 1.
DR Pfam: PF02752; Arrestin_C; 1.
DR PRINTS: PR00309; ARRESTIN.
DR ProDom: PD002099; Arrestin; 2.
FT NON_TER 1 1
FT NON_TER 245 245
FT SQ SEQUENCE 245 AA; 27038 MW; 86D8F4520115DA5F CRC64;

Query Match 63.6%; Score 1254; DB 2; Length 245;
Best Local Similarity 100.0%; Pred. No. 2.6e-90;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 129 LQGGEDNDGDCGVSYYVKIFAGESETDRTTRRSTVTLGIRKIQFAPTKOQOQCTLVK 188
Db 1 LQGGEDNDGDCGVSYYVKIFAGESETDRTTRRSTVTLGIRKIQFAPTKOQOQCTLVK 60
Qy 189 DPMLSPEGLIEVTLDKQLYHGERIGVNICIRNNSNMVKKIRAMVOGQVDVLFONGS 248
Db 189 DPMLSPEGLIEVTLDKQLYHGERIGVNICIRNNSNMVKKIRAMVOGQVDVLFONGS 120
Qy 249 YRNTVASIETSEGCPIQSGSLQKVMYLTPLLSNKKRGIALDGOIKRQDQCLASTTL 308
Db 249 YRNTVASIETSEGCPIQSGSLQKVMYLTPLLSNKKRGIALDGOIKRQDQCLASTTL 180
Qy 309 AOPDORDAFVGIIVSYAVKVKLFLGALGSELCAELPFILMHKPKGTAKVIAHDSQADVET 368
Db 309 AOPDORDAFVGIIVSYAVKVKLFLGALGSELCAELPFILMHKPKGTAKVIAHDSQADVET 240
Qy 369 PRODT 373


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Db 185 VKREYILKPNKIHLEASLDKELHYHGBESLSTVNHAIANNSSKTVKIKKIVSRQFADICLFS 244
Qy 246 NGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLISSNKGORGIALDGOIKRQDCLAST 305
Db 245 TAOYKCTVAEVESEDCGVABGFTLSKVFLLTPLANNKDKKMGALDQOLKHEBDNLASS 304
Qy 306 TLLAQPDQRDAFGVYIISAVKVKFLGALGELSABLPVLMHPKGTAKAVI 358
Db 305 TLLADPSGRENIGIIVQYKVKVLCITPLGDLVAELPFLIMHPKPDDEPVI 357

RESULT 10
ID Q70508_ANOGA PRELIMINARY; PRT; 398 AA.
AC Q70508; Q66G6;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 07-DEC-2004, sequence version 2.
DT 07-MAR-2006, entry version 14.
DE ENSANGP0000020628 (Arrestin 2-like protein Arr2).
GN Name=ARR2; ORFNames=ENSANG00000018139;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxId=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG MEDLINE=23159591; PubMed=14986925;
RX DOI=10.1046/j.1365-2583.2003.00450.x;
RA Merrill C.E., Pites R.J., Zwiebel L.J.;
RT "Molecular characterization of arrestin family members in the malaria
vector mosquito, Anopheles gambiae.";
RL Insect Mol. Biol. 12:641-650(2003).
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CC Distributed under the Creative Commons Attribution-NonDerivs license
CC -----
Db EMBL; AAB01008960; EMBL0755.2; -; Genomic DNA.
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Db GO; GO:0007600; P:sensory perception; IEA.
Db GO; GO:0007165; P:signal transduction; IEA.
Db InterPro; IPR000698; Arrestin.
Db InterPro; IPR011022; Arrestin_C.
Db InterPro; IPR011021; Arrestin_N.
Db PANTHER; PTHR11792; Arrestin; 1.
Db Pfam; PF003752; Arrestin_C; 1.
Db Pfam; PF00339; Arrestin_N; 1.
Db PRINTS; PR00309; ARRESTIN.
Db ProDom; PD00209; ARRESTIN.
Db PROSITE; PS00295; ARRESTINS; 1.
Db PROSITE; PS00295; ARRESTINS; 2.
SQ SEQUENCE 398 AA; 44536 MW; 73DD73FB34F01418 CRC64;

Query Match 51.8%; Score 1023; DB 2; Length 398;
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Matches 204; Conservative 65; Mismatches 111; Indels 10; Gaps 7;
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Db 119 SMAPSSVTLQAGEDDTPKPLGVEYAIKAHVGEESDGHKRSATVTLTKIQYAPVSRGR 178
Qy 181 Q-PCTVYKQPMLSRGLLEVTLLDKOLYHGERIGNVICIRNNSNMVKKIKVMQGV 239
Db 179 RLPSLSVSKGFTFSQGINLEVTLDRRIYHGEKIANIVTNSKRTVSIKCFVVOHC 238
Qy 240 DVVLFGNSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLISSNKGORGIALDGOIKRQD 299
Db 239 EYIMV-NAQPSKHIALETREGCITTPGASFTSFFLVPLASSNKGORGIALDHLKEDD 297
Qy 300 QCLASTLLAQPD-QRDAFGVYIISAVKVKFLGALGELSABLPVLMHPKGT--KAK 356
Db 298 VNLASSTLISEGKCPSDAMGIVISLRLVKLNCCTLGGELQTDVPLKMPNAPGSVERER 357
Qy 357 VIHADSQADVETPRQDT---IDQASVDFE 383
Db 358 VNALKKKKSIERRHYENSHVADDDNIVFE 387

RESULT 11
ID Q9V393_DROME PRELIMINARY; PRT; 470 AA.
AC Q9V393; DROME
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 29.
DE CG1487-PA (Kurtz arrestin) (LD31082p).
GN Name=Krz; ORFNames=CG1487; Dmel CG1487;
OS Drosophila melanogaster (Fruit Fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoeklin R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Baxu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Botkova D., Botchan M.R., Bouck J., Brockstein P., Brodtier P.,
RA Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., May A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasner K.,
RA Glodok A., Gong F., Gottrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasako F., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reiterer K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitskas R., Tector R., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
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RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [12]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Ceolinker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirekas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [13]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminiker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirekas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Ceolinker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
 RN [14]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminiker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Betencourt B.R., Ceolinker S.E., de Grey A.D.N.J., Dysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [15]
 RP NUCLEOTIDE SEQUENCE.
 RG Berkeley *Drosophila* Genome Project;
 RA Ceolinker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirekas R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [16]
 RP NUCLEOTIDE SEQUENCE.
 RG FLYBASE;
 RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.
 RN [17]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20341329; PubMed=10880488;
 RA Roman G., He J., Davis R.L.;
 RT "Nurx, a novel nonvisual arrestin, is an essential neural gene in
 RT *Drosophila*.";
 RL Genetics 155:1281-1295(2000).
 RN [18]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Berkely;
 RA Stapleton M., Brokstein P., Hong L., Abapany A., Carlson J.,
 RA Champe M., Chavez C., Dorese V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Parasas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Ceolinker S.;
 RT Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
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DR EMBL: AE003780; AAF57212.1; -; Genomic_DNA.
 DR EMBL: AF221066; AAF32365.1; -; Genomic_DNA.
 DR EMBL: AY118946; AAF50806.1; -; mRNA.
 DR HSSP: P17870; 1G4M.
 DR InAcC: Q9V393; -;
 DR FLYBASE: FBgn0040206; krz.
 DR GO: GO:0005515; F:Protein binding; IPI.
 DR InterPro: IPR000698; Arrestin.
 DR InterPro: IPR011022; Arrestin_C.
 DR InterPro: IPR011021; Arrestin_N.
 DR PANTHER: PTHR11792; Arrestin; 2.
 DR Pfam: PF02752; Arrestin_C_1.
 DR Pfam: PF00339; Arrestin_N_1.
 DR PRINTS: PR00309; ARRESTIN.
 DR PROSITE: PS00295; ARRESTINS; 1.
 SQ SEQUENCE 470 AA; 51237 MW; FEF954324007C26A CRC64;
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 Best Local Similarity 53.7%; Pred. No. 4,4e-70;
 Matches 187; Conservative 70; Mismatches 87; Indels 4; Gaps 3;
 QY 6 KVFKKCAPNGKVTLYMGKRPVDHVSQVEPIIDGIVYDDIYIRDNKRVFGQIVCSFPGYGR 65
 DB 48 RVEFKSSNSKRTIVYLGKDFVHVTHVDPIDGWVFIDPEYVKD-RKVFQVLAARFYGR 106
 QY 66 EEDVWGLNFOKEICLASQEIYPRPEKSKDEKQTKLERLYKLGUNAIPFTFNISPNAPS 125
 DB 107 EDDLVLGLTRKQDLYLAHEQIYF-PWQIDRPMRLDERLKKLGSPNAPFFVEYPCFA 165
 QY 126 SVTLQSGEDNDGPGCVSYVYKIFPAGESEFTRTHRSSTVTGLIRKIOFAPATKQGDPTCL 185
 DB 166 SVSIQAPPGGVGSCGVDELKAFVGENVEDKPKRNSVLTTRKMWYAPASKGEPSIE 225
 QY 186 VRKQFMSPSELELVTLKQLYLHGERIGVNICIRNNSKMWYKIKAMVQGVVDVLFQ 245
 DB 226 VSKPEPMKPKVNHIEATLDLDELTHHGKISVNVNHNANSRVTYKKIKVCYKQADICLFS 265
 QY 246 NGSYRNTVASLETSEGCPIPGSSLOKVMYLTPLTSSNKKORGIADLQGIKRDQCLAST 305
 DB 286 TAYKKSVAVAIESEDDGVAPGFITLSKVFELCPPLANNKKQKMGDALDQGHEDTNLASS 345
 QY 306 TLAAQPPQDAFGVITISYAVKVLFLGA--LGGELSAELPFVLMHPRP 351
 DB 346 TLITNPAQRSLGIMVYKVKVLLISSPLINDLVALEPFTLMHPRP 393
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 ARRH_LOCM1 STANDARD; PRT; 407 AA.
 AC P3122;
 DT 01-OCT-1993, integrated into UniProtKB/Swiss-Prot.
 DT 01-OCT-1993, sequence version 1.
 DT 07-FEB-2006, entry version 33.
 DE Arrestin homolog.
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthoptera; Orthoptera; Caelifera; Acridoidea;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (mRNA).
 RC TISSUE=Antenna;
 RX MEDLINE=9319955; PubMed=8452755; DOI=10.1016/0898-6568(93)90009-B;
 RA Raming K., Freitag J., Krieger J., Breer H.;
 RT "Arrestin-subtype in insect antennae.";
 RL Cell. Signal. 5:69-80(1993).
 CC -1-SIMILARITY: Belongs to the arrestin family.
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 CC EMBL: S57174; AAB25860.1; -; mRNA.
 DR PIR: A56607; A56607.

DR HSPP, P17870, 164M.
 DR InterPro: IPR000698; Arrestin.
 DR InterPro: IPR011022; Arrestin_C.
 DR InterPro: IPR011021; Arrestin_N.
 DR PANTHER: PTHR11792; Arrestin_1.
 DR Pfam: PF0752; Arrestin_C_1.
 DR Pfam: PF00339; Arrestin_N_1.
 DR PRINTS: PR00309; ARRESTIN.
 DR ProDom: PD002099; Arrestin_2.
 DR PROSITE: PS00295; ARRESTIN; 1.
 KM Sensory transduction.
 FT CHAIN 1 407 /Arrestin homolog.
 FT FTID:PRO_0000205221.
 SQ SEQUENCE 407 AA; 45543 MW; DEC28A3A534935BB CRC64;
 Query Match 50.4%; Score 993.5; DB 1; Length 407;
 Best Local Similarity 52.1%; Pred. No. 1.7e-69;
 Matches 202; Conservative 64; Mismatches 107; Indels 15; Gaps 8;
 QY 6 KVFKKCAENGKVTLYMGKRDVFDVHVSVEPIDGIVLDEYIRDNKRVFGQIVCSFRYGR 65
 DB 14 KVPKKTTPNGKVTYVIGKRPDIHDHVDPIDGIWVNDYLR-GRKVFQGLTTTYRYGR 72
 QY 66 EEDVWMLNPKQELCLASEQIVPREKSDKEQTLQELKKGSLNATPEFNISPNPAS 125
 DB 73 EEDVWMLKFTKEMVLAKQIVPQ-TKRMELTPIQERLMKKGNAFPFTFHPASSPS 131
 QY 126 SVTLQOQEDNDGDDPCGVSYVYKIFAGESEDTDRTHRSVTVLGIRKIQFAPTKQGO-PCT 184
 DB 132 SVTLQPGDDQKPLGVESYKVTWGDIAEKGRSNAVTLAIKQLQVAPTRGRGLSS 191
 QY 185 LVKRDPMLSPELELVTLDKQLYHGERIGVNICIRNNSNMKVKIKAMVQGVVLF 244
 DB 192 LVSKGFTEGQKINLEVTLDREIYHGEKLANVLIINNNSKTVNIKVYVQHCETVMV 251
 QY 245 QNGSRNTVALESTEGCPIQGSSLOQVMYITPLLSNKKRGIALGQIKRQDQGLAS 304
 DB 252 -NAQFSRHVASLETREGCPITPGASFTYFVLVPCAAANKRKYGIALDQGLKDDVNLAS 310
 QY 305 TTLTAQ-PPORDAFGVISYAVKVLPLGALGELSAELPFVLMHPKPGT----KAKYIH 359
 DB 311 STLVSQKQTTDAIVISYKRVLTNGCTLGLGLQTVDFPLHLPAQGTAREKQAI- 369
 QY 360 ADSQADVETFRQD---TIDQASVDFE 383
 DB 370 -KKMKSIERTRYENSCVAADDDNIVFE 396
 RESULT 13
 ARRB_DROME STANDARD; PRT; 401 AA.
 ID ARRB_DROME OSVSN6;
 AC P19107; integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1990, sequence version 2.
 DT 24-MAY-2004, entry version 54.
 DT 07-FEB-2006, entry version 54.
 DE Phosrestin-1 (Phosrestin 1) (Arrestin B) (Arrestin-2) (49 kDa
 DE arrestin-like protein).
 GN Name=Arr2; Synonyms=ArrB; ORFNames=CG5962;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCB1 TaxID=7227;
 RX MEDLINE=90232360; PubMed=2158671;
 RA Yamada T., Takeuchi Y., Konoori N., Kobayashi H., Sakai Y., Hotta Y.,
 RA Matsumoto H.,
 RT "A 49-kilodalton phosphoprotein in the Drosophila photoreceptor is an
 RT arrestin homolog."
 RT Science 248:483-486(1990).
 RN [2]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=Berkely;
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abell J.F., Agbayani A., An H.-U., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolintsov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burkova D., Busam M.A., Butler H., Cadien E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos R., Delcher A., Deng Z., Mays R.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howard T.J., Wei M.-H., Idegawa C.,
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kemnitz U.A., Ketchum K.A.,
 RA Jimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laekko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Metkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 RN [3]
 RN GENOME REANNOTATION.
 RX MEDLINE=22426069; PubMed=1253172;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitefield E.J., Bayraktaroglu L., Berman B.P.,
 RA Betencourt B.R., Celinker S.E., de Grey A.D.N.J., Dysdale R.A.,
 RA Harris N.L., Richter J., Ruse S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.,
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review."
 RL Genome Biol. 3:RESEARCH0083.22(2002).
 RN [4]
 RN PHOSPHORYLATION, AND PROBABLE FUNCTION.
 RX MEDLINE=91282780; PubMed=1905538;
 RA Matsumoto H., Yamada T.,
 RT "Phosrestin I and II: arrestin homologs which undergo differential
 RT light-induced phosphorylation in the Drosophila photoreceptor in
 RT vivo."
 RL Biochem. Biophys. Res. Commun. 177:1306-1312(1991).
 RN [5]
 RN PHOSPHORYLATION SITE SBR-366.
 RX MEDLINE=94242441; PubMed=8185954; DOI=10.1016/0896-6273(94)90309-3;
 RA Matsumoto H., Kurien B.T., Takagi Y., Kahn E.S., Kinumi T., Konoori N.,
 RA Yamada T., Hayashi F., Isono K., Pak W.L.,
 RT "Phosrestin I undergoes the earliest light-induced phosphorylation by
 RT a calcium/calmodulin-dependent protein kinase in Drosophila
 RT photoreceptors."
 RL Neuron 12:997-1010(1994).
 CC -!- FUNCTION: Probably plays an important role in the photoreceptor
 CC transduction.
 CC -!- TISSUE SPECIFICITY: Inner and outer segments, and the inner

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CC      -1- plexiform regions of the retina.
CC      -1- PTM: Phosphorylated upon light exposure.
CC      -1- SIMILARITY: Belongs to the arrestin family.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NonDerivs license
CC      -----
DR      EMBL: M32141; AAA28833.1; -; Genomic DNA.
DR      EMBL: AE003554; AA050380.1; -; Genomic DNA.
DR      PIR: A34856; A34856.
DR      HSSP: P17870; 1G4M.
DR      Ensemble: CG5962; Drosophila melanogaster.
DR      FlyBase: FBgn0000121; Arr2.
DR      BioCyc: DMEL-XXX-02:DMEL-XXX-02-015817-MONOMER; -.
DR      GO: GO:0005624; C:membrane fraction; IDA.
DR      GO: GO:0016028; C:rhabdomere; IDA.
DR      GO: GO:0005625; C:soluble fraction; IDA.
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DR      GO: GO:0016062; P:adaptation of rhodopsin mediated signaling; IMP.
DR      GO: GO:0016060; P:metarhodopsin inactivation; IMP.
DR      InterPro: IPR010022; Arrestin_C.
DR      InterPro: IPR011021; Arrestin_N.
DR      PANTHER: PTHR11792; Arrestin_N.
DR      Pfam: PF02752; Arrestin_C; 1.
DR      Pfam: PF00339; Arrestin_N; 1.
DR      PRINTS: PR00309; ARRESTIN.
DR      ProDom: PD002099; Arrestin; 2.
DR      PROSITE: PS00295; ARRESTINS; 1.
DR      Complete proteome: Phosphorylation; Sensory transduction; Vision.
DR      KW      Complete proteome; Phosphorylation; Vision.
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QY      61  FRYGREDEVMGKLPFOKELCLASEQIYPRPEKSDKEQTKLOERLLKKLGSNAIPFTFNIS 120
DB      60  YRYGREDEVMGVKFSKELLICREQIVPM-TNPMNEMTPMOEKLVRKLGSNAPFTFHP 118
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ID  ARRB_DROMI

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DT      01-NOV-1990, integrated into UniProtKB/Swiss-Prot.
DT      01-NOV-1990, sequence version 1.
DT      07-FEB-2006, entry version 41.
DE      Phosarrestin-1 (Phosarrestin I) (Arrestin B) (Arrestin-2) (49 kDa
DE      arrestin-like protein).
OS      Name=Arr2; Synonym=ArrB;
OS      Drosophila miranda (Fruit fly).
OC      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC      Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC      Ephydroidea; Drosophilidae; Drosophila.
RX      NCBI_Taxid=7229;
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RC      STRAIN=SZ04;
RX      MEDLINE=9101694; PubMed=2216789;
RA      Krishnan R., Ganguly R.;
RT      "Nucleotide sequence of the arrestin-like 49 kD protein gene of
RT      Drosophila miranda."
RL      Nucleic Acids Res. 18:5894-5894(1990).
CC      -1- FUNCTION: Undergoes light-induced phosphorylation, probably plays
CC      an important role in the photoreceptor transduction.
CC      -1- TISSUE SPECIFICITY: Inner and outer segments, and the inner
CC      plexiform regions of the retina.
CC      -1- SIMILARITY: Belongs to the arrestin family.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NonDerivs license
CC      -----
DR      EMBL: X54084; CA38019.1; -; Genomic DNA.
DR      PIR: S11566; S11566.
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DR      InterPro: IPR010022; Arrestin_C.
DR      InterPro: IPR011021; Arrestin_N.
DR      PANTHER: PTHR11792; Arrestin_N.
DR      Pfam: PF02752; Arrestin_C; 1.
DR      Pfam: PF00339; Arrestin_N; 1.
DR      PRINTS: PR00309; ARRESTIN.
DR      ProDom: PD002099; Arrestin; 2.
DR      PROSITE: PS00295; ARRESTINS; 1.
DR      Phosphorylation; Sensory transduction; Vision.
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Query Match      49.5%; Score 977.5; DB 1; Length 401;
Best Local Similarity 48.5%; Pred. No. 3e-68;
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QY      1  MVVNFKFKKCAPNGKVTLYWGRDPVDHVSVEPIDGIIVLDDDEYLRDNKRYFGQIVCS 60
DB      1  MVVSVKFKKATPNGKATFYLGRRDFIDHIDYCPDVGIVLVEPEYLYK-NRKVFGQLATT 59
QY      61  FRYGREDEVMGKLPFOKELCLASEQIYPRPEKSDKEQTKLOERLLKKLGSNAIPFTFNIS 120
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QY      181  Q-PCITLVKQFMLSPEGELELVTDKOLYLHGERIGVNICIRNNSNMKVKKIKAMVOGV 239
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GenCore version 5.1.8
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Total number of hits satisfying chosen parameters: 650591

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	885	44.9	382	2	US-09-880-137-8
5	885	44.9	409	2	US-09-880-137-4
6	880	44.6	409	2	US-09-880-137-7
7	853.5	43.3	401	2	US-09-949-016-8383
8	853.5	43.3	401	2	US-09-949-016-8384
9	780.5	39.6	388	2	US-09-880-137-6
10	779.5	39.6	388	2	US-09-880-137-5
11	767.5	38.9	317	2	US-09-949-016-9940
12	767.5	38.9	197	2	US-09-270-767-58832
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35	86.5	4.4	684	3	US-10-144-678A-775	Sequence 775, App
36	86.5	4.4	1030	2	US-09-091-117-2	Sequence 19232, A
37	86	4.4	657	2	US-09-248-796A-19232	Sequence 22, Appli
38	86	4.4	714	2	US-09-422-869-22	Sequence 867, App
39	86	4.4	714	2	US-09-538-092-867	Sequence 2916, Ap
40	85.5	4.3	800	2	US-09-583-110-2916	Sequence 4536, Ap
41	85.5	4.3	801	2	US-09-107-433-4536	Sequence 43701, A
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43	85	4.3	783	1	US-08-843-521-2	Sequence 2, Appli
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ALIGNMENTS

RESULT 1
US-09-880-137-3
; Sequence 3, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: NMI-131
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186, 706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-137-3

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RESULT 2

US-09-880-137-1
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; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: NMI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-880-137-1

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Db 66 EDDVLGLTRFKDLFVANNVQSFPPAPDKPRLTRLOERLLKKGNSAIPTFTNISPAAPS 125
Qy 126 SVTLQGEDNDGPGCVSYVYKIFAGESETRDRHRSVTTLGIKRIQFAPTKGQOQCTL 185
Db 126 SVTLQGPEDBTGKACGVYDVKAFCAENLEBKIKHNSVRLVIRKQYABERPGQPTAE 185
Qy 186 VRKDFMLSPGELEVLTDKQLYLHGERIGVNICIRNNSNMVKKIKAMVQGVVVLVQ 245
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Qy 246 NGSYRNTVSLSESGEPIOPGSSLOKVMYTLPLSSNKGRRGIALDGOIKRQDCLAST 305
Db 246 TAQYKCPVAMEEADD--TVAPSSTFCKVYTLTPFLANNRKRGLADGKLKHEDTNLASS 303
Qy 306 TLLAQPORDAFGVIIISYAVVKLFL--GALGELSA----ELPVLMPKPGTK--A 355
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Db 364 EVPEHETRPVDTNLIELDTND 383

RESULT 3
US-09-880-137-2
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; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: NMI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-137-2

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Qy 126 SVTLQGEDNDGPGCVSYVYKIFAGESETRDRHRSVTTLGIKRIQFAPTKGQOQCTL 185
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Qy 186 VRKDFMLSPGELEVLTDKQLYLHGERIGVNICIRNNSNMVKKIKAMVQGVVVLVQ 245
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Db 364 EVPEHETRPVDTNLIELDTND 383

RESULT 4
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; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: NMI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
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; LENGTH: 382
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
US-09-880-137-8

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Db      67 EDDLVLGLSFRKDLFIATYQAFPPVNPDPPTRLQDRLLKLGQHAHFFFTIPQNLPC 126
Qy      126 SVTLQGGEDNDGDCGVSYYVKIPAGESEDTDRHRSSTVTLGIRKIOFAPTKOGQOQCTL 185
      127 SVTLQGGEDTGKACGVDFEIRAFCAKSLBEKSHKRNVRVLRVQAPAPKBPQPSAE 186
Qy      186 VRKDFMLSPGELLEVTLDKQLYHGERIGVNICIRNNSKNVKKIKAMVOQGVNVLFQ 245
      187 TTRHFLMSDRSLHLEASLDKELVYHGEPLNVNVTNNSTKTKIKVSRQVADICLFS 246
Qy      246 NGSYRNTVASLETSEGCPIQGSSLOKVMYLTPLLSNKKORRGIALDGOIKRODQCLAST 305
      247 TAQYKCPVAQLEODD--QVSPSSTFCCKYTTITPLLSDRREKRGALDGLKHEDTNLASS 304
Db
Qy      306 TLAAQPDQDAFGVLIISYAVVKVFLGALGSELASALPFLVLMHPK 351
      305 TIVEGANKEVGLIVSYRVKVLV--SRGSDVSVELPFLVLMHPK 349
Db

```

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RESULT 5
US-09-880-137-4
; Sequence 4, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: NMI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-137-4

```

```

Query Match      44.9%; Score 885; DB 2; Length 409;
Best Local Similarity 48.3%; Pred. No. 1.6e-84;
Matches 167; Conservative 77; Mismatches 98; Indels 4; Gaps 3;

Qy      6 KVFKKCAPNGKVTLYMGKRDVFDHVSQVEPIDGIVLDEYIRDNKKVFGQIVCSFRYGR 65
      8 RVFKKSSPNCKLTLYLGRKDPVDHLDKVDVGVVLDVDDYKD--RKVFVTLTCAFRYGR 66
Db      66 EDEVMGLNFOKELCLASEQIYPRPEKSKQETKLOERLLKLGSNALPFTNISPNAPS 125
      67 EDDLVLGLSFRKDLFIATYQAFPPVNPDPPTRLQDRLLKLGQHAHFFFTIPQNLPC 126
Qy      126 SVTLQGGEDNDGDCGVSYYVKIPAGESEDTDRHRSSTVTLGIRKIOFAPTKOGQOQCTL 185
      127 SVTLQGGEDTGKACGVDFEIRAFCAKSLBEKSHKRNVRVLRVQAPAPKBPQPSAE 186
Db      186 VRKDFMLSPGELLEVTLDKQLYHGERIGVNICIRNNSKNVKKIKAMVOQGVNVLFQ 245
      187 TTRHFLMSDRSLHLEASLDKELVYHGEPLNVNVTNNSTKTKIKVSRQVADICLFS 246
Qy      246 NGSYRNTVASLETSEGCPIQGSSLOKVMYLTPLLSNKKORRGIALDGOIKRODQCLAST 305
      247 TAQYKCPVAQLEODD--QVSPSSTFCCKYTTITPLLSDRREKRGALDGLKHEDTNLASS 304
Db
Qy      306 TLAAQPDQDAFGVLIISYAVVKVFLGALGSELASALPFLVLMHPK 351
      305 TIVEGANKEVGLIVSYRVKVLV--SRGSDVSVELPFLVLMHPK 349
Db

```

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RESULT 6
US-09-880-137-7
; Sequence 7, Application US/09880137
; Patent No. 6640025

```

```

; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: NMI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; PRIOR FILING DATE: 2001-03-05
; CURRENT APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
US-09-880-137-7

```

```

Query Match      44.6%; Score 880; DB 2; Length 409;
Best Local Similarity 48.0%; Pred. No. 5.3e-84;
Matches 166; Conservative 77; Mismatches 99; Indels 4; Gaps 3;

Qy      6 KVFKKCAPNGKVTLYMGKRDVFDHVSQVEPIDGIVLDEYIRDNKKVFGQIVCSFRYGR 65
      8 RVFKKSSPNCKLTLYLGRKDPVDHLDKVDVGVVLDVDDYKD--RKVFVTLTCAFRYGR 66
Db      66 EDEVMGLNFOKELCLASEQIYPRPEKSKQETKLOERLLKLGSNALPFTNISPNAPS 125
      67 EDDLVLGLSFRKDLFIATYQAFPPVNPDPPTRLQDRLLKLGQHAHFFFTIPQNLPC 126
Qy      126 SVTLQGGEDNDGDCGVSYYVKIPAGESEDTDRHRSSTVTLGIRKIOFAPTKOGQOQCTL 185
      127 SVTLQGGEDTGKACGVDFEIRAFCAKSLBEKSHKRNVRVLRVQAPAPKBPQPSAE 186
Db      186 VRKDFMLSPGELLEVTLDKQLYHGERIGVNICIRNNSKNVKKIKAMVOQGVNVLFQ 245
      187 TTRHFLMSDRSLHLEASLDKELVYHGEPLNVNVTNNSTKTKIKVSRQVADICLFS 246
Qy      246 NGSYRNTVASLETSEGCPIQGSSLOKVMYLTPLLSNKKORRGIALDGOIKRODQCLAST 305
      247 TAQYKCPVAQLEODD--QVSPSSTFCCKYTTITPLLSDRREKRGALDGLKHEDTNLASS 304
Db
Qy      306 TLAAQPDQDAFGVLIISYAVVKVFLGALGSELASALPFLVLMHPK 351
      305 TIVEGANKEVGLIVSYRVKVLV--SRGSDVSVELPFLVLMHPK 349
Db

```

```

RESULT 7
US-09-949-016-8383
; Sequence 8383, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8383
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8383

```

Query Match	43.3%	Score 853.5	DB 2	Length 401
Beet Local Similarity	46.1%	Pred. No.3.3e-81		
Matches 170	Conservative	75	Mismatches 111	Indels 13
			Gaps	5
Qy	17	VTLYWKGKDFVNVHVGSEVPIDIGVLDDEYIDRNRKVFQIYVCSFRFYGREEDVMGILNQ	76	
Db	1	LTIVYIGKRDVVDHIDLVDVGDGVLDVDPYLYNE-RVVYVTLTICAFYRGYBDDLDVGLTR	59	
Qy	77	KELCLASQIYRPREKSDKEQTKLOERLLIKLUSNAIPTFENISPNAPSSVTLQOGEDDN	136	
Db	60	KDLFVANNOSPEPPAPEDKKPLTRLERLLIKUGENHAYPEPTFELIPMLPSCSVTLQOPSEBDT	119	
Qy	137	GDPCGVSYVYKIFAGESEITDRTHRSTVTLGIRKIOFAPTKQOQPCITLVKROFMLSPEG	196	
Db	120	GKACGVYDEVKAFCEHLENLEEKIKRNSVYLVRKQVYABERPSQPTAETTRQFLMSDKR	179	
Qy	197	LELEVTLDKQVLYHGERIGVNI CIRNNSKNMYKKIKAMYQOQGVVYL FONGSYRNTVASL	256	
Db	180	LHLEASLDKEIKYYHGEPI SVNHVHTNNTKTKVKKISVRQYADICLFNTAQYKCVAME	239	
Qy	257	ETSECCPQOPGSLQKMWLTPLLSSNKRGRGALDGOQKROQCCLASTTLAQPQRDA	316	
Db	240	EADD--TVAPSSPTFCVYVTLTPPLANNRKRKGIALDGKIKHEBTINLASSSTLLEGANREI	297	
Qy	317	FGVILSYAVKVLFL--GALGELSIA----ELPFVLMHPKPGTK--AKVITADSQADV	366	
Db	298	LGIIVSYKVKVLLVVSRRGLLDGLASSDVAVELPFLTLMHPKKEEPRPHREVPENERPVDT	357	
Qy	367	ETFRQDITD	375	
Db	358	NLIEDTND	366	

```
RESULT 8  
US-09-949-016-8384  
Sequence 8384, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
. APPLICANT: VENTER, J. Craig et al.  
. TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
. FILE REFERENCE: CLOO01307  
. CURRENT APPLICATION NUMBER: US/09/949,016  
. PRIOR FILING DATE: 2000-04-14  
. PRIOR APPLICATION NUMBER: 60/241,755  
. PRIOR FILING DATE: 2000-10-20  
. PRIOR APPLICATION NUMBER: 60/237,768  
. PRIOR FILING DATE: 2000-10-03  
. PRIOR APPLICATION NUMBER: 60/231,498  
. PRIOR FILING DATE: 2000-09-08  
. NUMBER OF SEQ ID NOS: 207012  
. SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8384  
LENGTH: 401  
TYPE: PRT  
. ORGANISM: Human  
US-09-949-016-8384
```

Query Match 43.3%; Score 853.5; DB 2; Length 401;
Best Local Similarity 46.1%; Pred. No. 3,3e-81;

	Matches	Conservative	% Matches	Indels	Gaps
Dy	17	VTLVWGRDPVDHVSQVEPIDGIVLVDDEXEYIRDNKRVFGQIYCSFRRYGREDEVMGLNFQ	76	: :: :	:
Dd	1	LTVLVIGKRDFVDHIDLVPDVGVLVDPEFLKE-RRYYVTLLCAFFRYGREDDLVLTGTFR	59	:: :	:: :
Dz	77	KELCLASSEDGYRPPEKSDEQTQLQERLLKKGSNAPIPTFNISPNASSVTLQQGEDND	136	: :: :	:
Df	60	KDLFWANVOSEPPAPEDDKPLFTLRQLRLIKKGAEHYAYPEETFEIPMLPCSVTLPQGPEDT	119	: :: :	:
Dg	137	GDPCGVSYVKLFAGSESFDTRHRASTVTLGITKIQAIFPKQQOQCCTLVRKDPMLSPGE	196	: :: :	:
Dc	120	GACCGVDYEVAFCENLEEKIHKNRSVRLVIARKVVYAERPBPQPATAETTROFLWSDKP	179	: :: :	:

QY	197	LELEVTLDKOLYLHEERIGVNI	CIRNNNNKMYKKT	KAMVQGV	DVVLFPONGSR	FRNTV	ASL	256		
Db	180	LHLEASLPEKLEYHGEPI	SVNHNVTNNNTKYK	KI	ISVQVADICL	FNTA	QYKCFVAME	239		
QY	257	ETSECCPIQPGSSLDQ	KWYLPPLBSN	KORRGIALDGOI	KPODOCLAST	TLTLAOP	QORDA	316		
Db	240	EADD--TVA	PSSTFECKVYTLT	LPFLANNKEKRG	IALDGLKHE	DTNLAS	TLREGANREI	297		
QY	317	FGVIIISYAVKYL	FLP--GALG	ELSA---ELP	VLMHPKGT	K---AK	VHAD	SOADV	366	
Db	298	LGIISYKVKV	LVVSRGGLGLD	LASSDVAVEL	PFLTMHPK	KEBPE	PHRE	BPENET	PVDT	357
QY	367	ETFR	ODTID	375						
Db	358	NLI	ELDTND	366						

```

RESULT 9
US-09-880-137-6
; Sequence 6, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Bernstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-137-6

```

Query Match	39.6%	Score 780.5	DB 2	Length 388
Best Local Similarity	42.7%	Pred. No. 1.6e-73		
Matches	166	Conservative	79	Mismatch 125, Indels 19, Gaps 7
QY	6	KVFKKCAPNGKTLVYMKRDPVDHVSQVPIIGIIVLDDEDIYRDNKVFQGIYCSFRYGR	65	
DB	3	KVFKTTSSNGKSLIYLGRDPVDHDIYPERIDGVLVDEIYK - CKLFLMLTCARYYR	61	
QY	66	BEDEVGILNFOKECLCLASEQIYPRBEKSDK - EOTKLOERLLKKLGSSNAIPIFTFNISPNAP	124	
DB	62	DLLEIGLTFRRKDLIVQTLQVLPAPSSSPQALTLVQELHLKLGNAVPIFLQMTNLP	121	
QY	125	SSVTLQOGBDDNDGDCGVSYYVKIIFAGESEDTNRHSRVTLTGIRIQAPTRQGOQPC	184	
DB	122	CSVTLQOGBEDBKGCGLIDFEYKSCAENPETSCKADYRLVYRKVQYAPRAGGPRSA	181	
QY	185	LVKRDPMLSPEGLELVTLDKOLYHGERIGNVICIRNNSNKKVKKIKAMVOGVNVLE	244	
DB	182	QIRRFLLSAQGLQVAMWDRVHYHGEPISYNVSINNCTNKVIKKIKITSVDITDVVLY	241	
QY	245	QNGSIRNTVYASLETSEGCPIQPGSSIQKMYTLTPLLSSKKQRGITLDDQIKRODCSLA	304	
DB	242	SLDKTKTVFIOEFTE - TVANSSFSPOSFAVTPILAAQCQRGLADKGLKIEDINLMS	299	
QY	305	TTLLAQPORDAFGVLIYAAVVKVSKFL - GALVGETLSA - - - - - ELRFVLMHPRKPTKAKV	357	
DB	300	STIIRPGMDKELLGLIVSYKVRVNLMSGCGGILGDTLADVGVLELPLVLIHPRKSHDA -	358	
QY	358	IHAUSDADV - - - ETRQDTITDQASVDPE	383	
DB	359	- - - - - SSEDIIVEEFTTRKEEESQKQVEAE	383	

RESULT 10

```

US-09-880-137-5
; Sequence 5, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: MN-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; LENGTH: 388
; TYPE: PR
; ORGANISM: Homo sapiens
US-09-880-137-5

Query Match
Best Local Similarity 42.4%; Score 779.5; DB 2; Length 388;
Matches 165; Conservative 80; Mismatches 125; Indels 19; Gaps 7;

QY 6 KVFKKCANPCKVTLTGMKRDVHDVSGVEPIDGIYVLDDEYIRNKRKVFQGVICVFRYGR 65
DB 3 KVFKTSNGKLSIYLGKRDVHDVDPIDGVVLDVPEYIK-CRKLFWMLTCAFRYGR 61
QY 66 EDEVMGLNPOKELCLASEQIYPRPEKSDK-EQTLORLKLKGSNAPIPTFNISPNAP 124
DB 62 DDELYTGLTFRKDLVYQTLQVPAESSPOGLTYLQERLHKLKDNAPFLQVMTLP 121
QY 125 SVTLQGEDNDGDCGVSYVYKIFAGESETDRTRRSTVTLGIRKIOFAPTKOQOQPT 184
DB 122 CSVTLOPGEEDGKACGVDFEIRACAKSLBKSHKRSVRLVIRKQVAPKPGQPSAE 181
QY 185 LVKDFMLSPGELLEVTLDKQYLHGERIGVNICIRNNSNMVKKIRAMVOQGVYVLF 244
DB 182 QTRIFLLSAOPLQIQAAMWDRVHNGEPISVNVNCTKNVKKIKISVDQITDVVLY 241
QY 245 QNGSRNTVASLETSEGCPIQGSLSLOKMYLTPLSSNKGORGIADGOIKRODOCLAS 304
DB 242 SLDKYTKVFTIOEFTE--TVANSSFSQSPAVTPIILASCOGRGIALDGLKHEDTNLAS 299
QY 305 TTLAOPORDAFGVIIISYAVKVKLFL--GALGELSA-----ELPVLMPKPGTKAKV 357
DB 300 STIRPGMDKELGLIVSGYKRVNLMVSCGILGDLTASDVGVLPVLVHPKPSHEAA- 358
QY 358 IHADSQADV--ETFRDITIDQASVDFE 383
DB 359 -----SSEDIIVIEFTRKGEESQKAVEAE 383

RESULT 11
US-09-949-016-9940
; Sequence 9940, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9940

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; LENGTH: 315
; TYPE: PR
; ORGANISM: Human
US-09-949-016-9940

Query Match
Best Local Similarity 48.0%; Score 767.5; DB 2; Length 315;
Matches 145; Conservative 66; Mismatches 88; Indels 3; Gaps 2;

QY 6 KVFKKCANPCKVTLTGMKRDVHDVSGVEPIDGIYVLDDEYIRNKRKVFQGVICVFRYGR 65
DB 8 RVFKSSPNCKLTYLTKRDVFDHLDKYDVPDGVVLDVPLKD-RKVFVLTCAFRYGR 66
QY 66 EDEVMGLNPOKELCLASEQIYPRPEKSDKQETLORLKLKGSNAPIPTFNISPNAPS 125
DB 67 EDLDVLGSFPRKDLFIATYQAFPPVPPRPPIRLQDRLLKGLQCHHPFFFTIPQNLPC 126
QY 126 SVTLQGEDNDGDCGVSYVYKIFAGESETDRTRRSTVTLGIRKIOFAPTKOQOQPTL 185
DB 127 SVTLQPEPEDGKACGVDFEIRACAKSLBKSHKRSVRLVIRKQVAPKPGQPSAE 186
QY 186 VRKDFMLSPGELLEVTLDKQYLHGERIGVNICIRNNSNMVKKIRAMVOQGVYVLFQ 245
DB 187 TTRHFLMSDRSLHLEASLDKELYHGEPLNVAVHTNNTSTYKIKIVSVQVADICLFS 246
QY 246 NGSRNTVASLETSEGCPIQGSLSLOKMYLTPLSSNKGORGIADGOIKRODOCLAS 305
DB 247 TAOYKCPVAQLEQDD--QVSPSTFCVKVYTTITPLSDRERKRGALDGLKHEDTNLAS 304
QY 306 TL 307
DB 305 TM 306

RESULT 12
US-09-270-767-58832
; Sequence 58832, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 58832
; LENGTH: 197
; TYPE: PR
; ORGANISM: Drosophila melanogaster
US-09-270-767-58832

Query Match
Best Local Similarity 49.6%; Score 316; DB 2; Length 197;
Matches 59; Conservative 25; Mismatches 33; Indels 2; Gaps 1;

QY 235 VOQGVYVLPONGSTRTNTVASLETSEGCPIQGSLSLOKMYLTPLSSNKGORGIADGO 294
DB 2 VROFADICLFSTAOYKSVVAIESEDCGVAPGFTLSYVFLCPILANNKOKMGIALDGO 61
QY 295 IKRODOCLASITTLAOPORDAFGVIIISYAVKVKLFLGA--LGGELSAELPFLVMPK 351
DB 62 LKHEDTNLASITLTPNQRSGLGMVYKVKVLLISSPLNDGVVALEPFLTMHPRP 120

RESULT 13
US-09-270-767-43475
; Sequence 43475, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094

```

```

: CURRENT APPLICATION NUMBER: US/09/270,767
: CURRENT FILING DATE: 1999-03-17
: NUMBER OF SEQ ID NOS: 62517
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 43975
: LENGTH: 475
: TYPE: CPT
: ORGANISM: Drosophila melanogaster
: FEATURE:
: OTHER INFORMATION: Xaa means any amino acid.
: US-09-270-767-43475

```

Query Match	16.0%;	Score 316;	DB 2;	Length 475;
Best Local Similarity	49.6%;	Pred. No. 2.7e-24;		
Matches 59;	Conservative 25;	Mismatches 33;	Indels 2;	Gaps 1;

Dy **235** VQGVADVLT.FONGSIRNTVASLETSEGCPIPGSSLOKVMYVLPPLSSNKQRGIALDQG 294
 | : | : | : | : | : | : | : | : | : | : | : | :
Db **280** VRGFADICLFSTAGYKSVAIEISEEGCQVAPGTLSKFELCPLLANNKDKGALDDQG 339

OY 295 IKRDQCLASTTLLAQRDQRDAFGVITISYA VKKKLFLGA--LGSELSAELPFLVMHPK 351
 :|::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 340 LKHEDTNLASTLTINPAQRSGLIMHYKVKKYLSSRPLNDLVAEIPFTLMHPRK 398

```

RESULT 14
US-09-270-767-32381
; Sequence 32381, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32381
; LENGTH: 137
; TYPE: PR1
; ORGANISM: Drosophila melanogaster
; US-09-270-767-32381

```

Query Match	11.4%;	Score 225;	DB 2;	Length 137;
Best Local Similarity	42.6%;	Pred. No. 1.5e-15;		
Matches	52;	Conservative	26;	Mismatches 38;
			Indels	6;
			Gaps	4;

```
QY      6 KVFKKCAPNGKVTLYMGKRDPEVDHVSQVEP--IDGIIVLDEDEYTRDNRKVFGQICSFPR 63
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     19 RYVKKTSFNCVLTLYLPTREIT--LTGNNPSVLRGIVYVDPKALQGYR--VYAQLTLTFRR 75
```

```
Oy      64 GREDEVMGINFQKELCLASQIYPPPEKSDEQ-TLKQERLLIKKLGSNAIPPTENISPN 122
       ||::|||:::||::||::||::||::||::||::||::||::||::||::||::||
Db      76 GREDEVMGIRFCNEAISMSLHQIWPRLEPPTESLSPLQALMKRLDGAHPFTTSSLSY 135
```

QY	123	AP	124
Db	136	AP	137

```

RESULT 15
US-09-270-767-47598
; Sequence 47598, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-0594
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47598

```

```

; LENGTH: 137
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-47598

```

Query Match	11.4%;	Score 225;	DB 2;	Length 137;
Best Local Similarity	42.6%;	Pred. No. 1.5e-15;		
Matches	52;	Conservative	26;	Mismatches 38;
			Indels	6;
			Gaps	4;

QY 6 KVFKECAAGNGKVLTYMKRDFVHDVSGVEP--IDGIIVLDDDEYLRDNRFKFGGIVCSFSFY 63
 :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
 Db 19 RVVKKTSPNCVLLTLYLPTRREIT--LTGNPPSVLGIVVDPAKIQGYR-VYAQLTLTFRY 75

```

Qy      64 GREDEVMGINFQKELCLASEQIYRPEREKDEQ-TKLQERLLKKLGSMNAIPFTFNISPN 122
      ||::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db      76 GREDEVMGIRFCNEAIMSLHQIMWRLEEPTPESSPLQEAIMKRGDGAHPFTLSLSY 135

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Qy	123 AP 124
	136 AP 137
Db	

Search completed: May 20, 2006, 22:52:44
Job time : 29 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 20, 2006, 23:03:28 / Search time 181 Seconds
(without alignments)
980.173 Million cell updates/sec

Title: US-10-056-405-2

Sequence: 1 MYNFKYFKKCAPNGKVTLY.....ADVETFRDITDQASVDFE 383

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /EMC_Celettera_SIDS3/ptodata/2/pubppaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celettera_SIDS3/ptodata/2/pubppaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celettera_SIDS3/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celettera_SIDS3/ptodata/2/pubppaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celettera_SIDS3/ptodata/2/pubppaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celettera_SIDS3/ptodata/2/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1973	100.0	383	4	US-10-094-240-2
2	1973	100.0	383	4	US-10-056-405-2
3	1973	100.0	383	5	US-10-954-778-238
4	1384	70.1	364	5	US-10-745-237-18
5	1384	70.1	364	6	US-11-097-143-12000
6	1023	51.8	398	4	US-10-094-240-25
7	1023	51.8	398	5	US-10-954-778-241
8	1002	50.8	470	6	US-11-097-143-1314
9	982.5	49.8	401	4	US-10-094-240-27
10	982.5	49.8	401	6	US-11-097-143-12684
11	907.5	46.0	410	3	US-09-880-137-3
12	907.5	46.0	410	3	US-09-880-137A-3
13	903.5	45.8	418	3	US-09-880-137-1
14	903.5	45.8	418	3	US-09-800-137A-1
15	903.5	45.8	452	4	US-10-038-010-52
16	900.5	45.6	418	4	US-10-043-487-348
17	900.5	45.6	418	5	US-10-745-237-216
18	897.5	45.5	418	5	US-09-880-137-2
19	897.5	45.5	418	5	US-09-800-137A-2
20	890	45.1	369	5	US-10-450-763-43933
21	885	44.9	382	3	US-09-880-137-8
22	885	44.9	382	3	US-09-880-137A-8
23	885	44.9	409	3	US-09-880-137-4
24	885	44.9	409	3	US-09-800-137A-4
25	885	44.9	479	6	US-11-170-123-3
26	885	44.9	492	6	US-11-170-123-4
27	880	44.6	409	3	US-09-880-137-7

28	880	44.6	409	3	US-09-800-137A-7	Sequence 7, Appli
29	869.5	44.1	410	4	US-10-038-010-54	Sequence 54, Appl
30	865	43.8	454	4	US-10-369-493-6702	Sequence 6702, Ap
31	780.5	39.6	388	3	US-09-880-137-6	Sequence 6, Appli
32	780.5	39.6	388	3	US-09-800-137A-6	Sequence 6, Appli
33	779.5	39.5	388	3	US-09-880-137-5	Sequence 5, Appli
34	779.5	39.5	388	3	US-09-800-137A-5	Sequence 5, Appli
35	379.5	19.2	466	4	US-10-722-357-31	Sequence 31, Appl
36	361.5	18.3	212	4	US-10-106-698-4673	Sequence 4673, Ap
37	351.5	17.8	456	6	US-11-097-143-3633	Sequence 3633, Ap
38	173	8.8	65	3	US-09-864-761-45375	Sequence 45375, A
39	136.5	6.9	335	6	US-11-097-143-3657	Sequence 3657, Ap
40	111	5.6	38	3	US-09-864-761-40768	Sequence 40768, A
41	108.5	5.5	612	5	US-10-945-678-16	Sequence 16, Appl
42	102	5.2	36946	5	US-10-840-512-155	Sequence 15, Appl
43	101.5	5.1	632	5	US-10-945-678-15	Sequence 15, Appl
44	100.5	5.1	638	5	US-10-733-969A-23	Sequence 23, Appl
45	99.5	5.0	342	6	US-11-097-143-15519	Sequence 15519, A

ALIGNMENTS

RESULT 1									
US-10-094-240-2									
Sequence 2, Application US/10094240									
Publication No. US20030082637A1									
GENERAL INFORMATION:									
APPLICANT: ZWIEBEL, LAURENCE J.									
TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF									
FILE REFERENCE: N8289									
CURRENT APPLICATION NUMBER: US/10/094,240									
CURRENT FILING DATE: 2001-03-08									
PRIOR APPLICATION NUMBER: 10/056,405									
PRIOR FILING DATE: 2002-01-24									
PRIOR APPLICATION NUMBER: 60/264,649									
PRIOR FILING DATE: 2001-01-26									
NUMBER OF SEQ ID NOS: 27									
SOFTWARE: PatentIn Ver. 2.1									
SEQ ID NO 2									
LENGTH: 383									
TYPE: PRT									
ORGANISM: Anopheles gambiae									
US-10-094-240-2									
Query Match									
Best Local Similarity 100.0%; Score 1973; DB 4; Length 383;									
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MYNFKYFKKCAPNGKVTLYGKRD	FVDHVS	GVEPIGIV	VLLDDEYIR	DNKRV	FGQIVCS	60	
DB	1	MYNFKYFKKCAPNGKVTLYGKRD	FVDHVS	GVEPIGIV	VLLDDEYIR	DNKRV	FGQIVCS	60	
QY	61	FRYREDEWGLNFKOKELASBOIYR	PEKSDKEQTKOERLL	KKLSNAI	PFTFNIS	120			
DB	61	FRYREDEWGLNFKOKELASBOIYR	PEKSDKEQTKOERLL	KKLSNAI	PFTFNIS	120			
QY	121	PNABSVTLQGGEDNDGDCGVS	YIVKIFAGESETDR	THRSSTYTLTGIRKI	QFAPTRQGO	180			
DB	121	PNABSVTLQGGEDNDGDCGVS	YIVKIFAGESETDR	THRSSTYTLTGIRKI	QFAPTRQGO	180			
QY	181	OPTLYVRDPMFLSGEILEYTL	LDKOLYHGERIGVNI	CINNSNKWVKIKAMVQGV	240				
DB	181	OPTLYVRDPMFLSGEILEYTL	LDKOLYHGERIGVNI	CINNSNKWVKIKAMVQGV	240				
QY	241	VLFONGSYRNTVASLETSE	CGPIQPGSSLOKWMYLP	PLSSNQRGIALDGOIKRDO	300				
DB	241	VLFONGSYRNTVASLETSE	CGPIQPGSSLOKWMYLP	PLSSNQRGIALDGOIKRDO	300				
QY	301	CIASSTLLAOPDQDRAFGV	ITISYAVKVLFTGALGGEIS	ASLPVLMHPKRGTAQVTHA	360				
DB	301	CIASSTLLAOPDQDRAFGV	ITISYAVKVLFTGALGGEIS	ASLPVLMHPKRGTAQVTHA	360				

QY 361 DSQADVETFRQDRTIDQASVDPE 383
|||
Db 361 DSQADVETFRQDRTIDQASVDPE 383

RESULT 2

US-10-056-405-2
; Sequence 2, Application US/10056405
; Publication No. US20030166013A1
; GENERAL INFORMATION:
; APPLICANT: ZWIEBEL, LAURENCE J.
; TITLE OF INVENTION: MOSQUITO OLFATORY GENES, POLYPEPTIDES, AND METHODS OF
; TITLE OF INVENTION: MOSQUITO OLFATORY GENES, POLYPEPTIDES, AND METHODS OF
; FILE REFERENCE: N7841
; CURRENT APPLICATION NUMBER: US/10/056,405
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/264,649
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Anopheles gambiae
US-10-056-405-2

Query Match 100.0%; Score 1973; DB 4; Length 383;
Best Local Similarity 100.0%; Pred. No. 66-176;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNFKVFKKCAPNGKVTLYMGKDFVDHSGVPEPIDGIIVLDDDEYIRDNKRVFGQIVCS 60
|||
Db 1 MYNFKVFKKCAPNGKVTLYMGKDFVDHSGVPEPIDGIIVLDDDEYIRDNKRVFGQIVCS 60
QY 61 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEOTKLOERLLKLGSNALPFTFNIS 120
|||
Db 61 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEOTKLOERLLKLGSNALPFTFNIS 120
QY 121 PNPASSVTLQGGEDDNGDPCGVSYVVKIFAGESETDTRHRSVTYLGIRKIQFAPTKQGG 180
|||
Db 121 PNPASSVTLQGGEDDNGDPCGVSYVVKIFAGESETDTRHRSVTYLGIRKIQFAPTKQGG 180
QY 181 QPCTLVKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKKVKKIKAMVQGGVD 240
|||
Db 181 QPCTLVKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKKVKKIKAMVQGGVD 240
QY 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKORRGIALDGOIKRQDQ 300
|||
Db 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKORRGIALDGOIKRQDQ 300
QY 301 CLASTTLAOPDORDARGVIIISYAVKVLFLGALGELSALPFLVLMHPKGTAKAYIHA 360
|||
Db 301 CLASTTLAOPDORDARGVIIISYAVKVLFLGALGELSALPFLVLMHPKGTAKAYIHA 360
QY 361 DSQADVETFRQDRTIDQASVDPE 383
|||
Db 361 DSQADVETFRQDRTIDQASVDPE 383

RESULT 3

US-10-954-778-238
; Sequence 238, Application US/10954778
; Publication No. US20050153368A1
; GENERAL INFORMATION:
; APPLICANT: ZWIEBEL, LAURENCE J.
; TITLE OF INVENTION: METHOD OF IDENTIFYING CHEMICAL AGENTS WHICH STIMULATE
; TITLE OF INVENTION: ODORANT RECEPTORS OF SENSORY NEURONS
; FILE REFERENCE: N1125
; CURRENT APPLICATION NUMBER: US/10/954,778
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 10/056,405
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/264,649

; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 238
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Anopheles gambiae
US-10-954-778-238

Query Match 100.0%; Score 1973; DB 5; Length 383;
Best Local Similarity 100.0%; Pred. No. 66-176;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNFKVFKKCAPNGKVTLYMGKDFVDHSGVPEPIDGIIVLDDDEYIRDNKRVFGQIVCS 60
|||
Db 1 MYNFKVFKKCAPNGKVTLYMGKDFVDHSGVPEPIDGIIVLDDDEYIRDNKRVFGQIVCS 60
QY 61 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEOTKLOERLLKLGSNALPFTFNIS 120
|||
Db 61 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEOTKLOERLLKLGSNALPFTFNIS 120
QY 121 PNPASSVTLQGGEDDNGDPCGVSYVVKIFAGESETDTRHRSVTYLGIRKIQFAPTKQGG 180
|||
Db 121 PNPASSVTLQGGEDDNGDPCGVSYVVKIFAGESETDTRHRSVTYLGIRKIQFAPTKQGG 180
QY 181 QPCTLVKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKKVKKIKAMVQGGVD 240
|||
Db 181 QPCTLVKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKKVKKIKAMVQGGVD 240
QY 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKORRGIALDGOIKRQDQ 300
|||
Db 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKORRGIALDGOIKRQDQ 300
QY 301 CLASTTLAOPDORDARGVIIISYAVKVLFLGALGELSALPFLVLMHPKGTAKAYIHA 360
|||
Db 301 CLASTTLAOPDORDARGVIIISYAVKVLFLGALGELSALPFLVLMHPKGTAKAYIHA 360
QY 361 DSQADVETFRQDRTIDQASVDPE 383
|||
Db 361 DSQADVETFRQDRTIDQASVDPE 383

RESULT 4

US-10-745-237-18
; Sequence 18, Application US/10745237
; Publication No. US20050227301A1
; GENERAL INFORMATION:
; APPLICANT: Cycloacel Limited
; APPLICANT: Glover, David
; APPLICANT: Frenz, Lisa
; APPLICANT: Midgley, Carol
; TITLE OF INVENTION: Cell Cycle Progression Proteins
; FILE REFERENCE: P015819MO CYK
; CURRENT APPLICATION NUMBER: US/10/745,237
; CURRENT FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: US 60/439,123
; PRIOR FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 60/468,402
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: AAF53644
; FEATURE:
; OTHER INFORMATION: GI:7298421
US-10-745-237-18

Query Match 70.1%; Score 1384; DB 5; Length 364;

Best Local Similarity 70.3%; Pred. No. 9.4e-121;
Matches 258; Conservative 51; Mismatches 54; Indels 4; Gaps 2;

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QY 1 MVAVFYFKKCAPNGKATLYMGKRDVFDHVSQVEPIDIGIVLDDDEYIRDNKRVFGQIVCS 60
DB 1 MVAVFYFKKCAPNGKATLYMGKRDVFDHVSQVEPIDIGIVLDDDEYIRDNKRVFGQIVCS 60
QY 61 FRYGREDEWGLNFGKELCLASQIYPRPEKSKDEQTKQERLLKKLGSNAIPFTFNIS 120
DB 61 FRYGREDEWGLNFGKELCLASQIYPRPEKSKDEQTKQERLLKKLGSNAIPFTFNIS 120
QY 121 PNASSVTLQGGEDDNGDPCGVSYVVKIFAGESETDTHRRSTVTLGIRKIQAPTKOGQ 180
DB 121 PNASSVTLQGGEDDNGDPCGVSYVVKIFAGESETDTHRRSTVTLGIRKIQAPTKOGQ 180
QY 120 PSSPASVTLQGXKSDSQPCGVQYFVKIFGDSDCDRSHRSTINLGIKRVQYAPTKOGI 179
DB 120 PSSPASVTLQGXKSDSQPCGVQYFVKIFGDSDCDRSHRSTINLGIKRVQYAPTKOGI 179
QY 181 QPCTVVRKDFMLSPGSELEVTLDKQLYLHGERIGVNICIRNNSNKKVKKIKAMVQOGVD 240
DB 181 QPCTVVRKDFMLSPGSELEVTLDKQLYLHGERIGVNICIRNNSNKKVKKIKAMVQOGVD 240
QY 180 QPCTVVRKDFMLSPGSELEVTLDKQLYLHGERIGVNICIRNNSNKKVKKIKAMVQOGVD 239
DB 180 QPCTVVRKDFMLSPGSELEVTLDKQLYLHGERIGVNICIRNNSNKKVKKIKAMVQOGVD 239
QY 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOQWYVTLPLSSNKKORGIALLDQIKRODQ 300
DB 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOQWYVTLPLSSNKKORGIALLDQIKRODQ 300
QY 240 VVLFQNGQFRNTIAFMETSEGCPLNPGSSLOQWYVTLPLVANCDBAGIAVEGDIKRKDT 299
DB 240 VVLFQNGQFRNTIAFMETSEGCPLNPGSSLOQWYVTLPLVANCDBAGIAVEGDIKRKDT 299
QY 301 CLASTTLLAOPDQDARGVIIISYAVKVLFLGALGELSAELPVLMPKPKGTAKAYIHA 360
DB 301 CLASTTLLAOPDQDARGVIIISYAVKVLFLGALGELSAELPVLMPKPKGTAKAYIHA 360
QY 300 ALASTTLLASQDARDADFGIIVSYAVKVLFLGALGELCAELPFLMHPKPSRKAQL--- 356
DB 300 ALASTTLLASQDARDADFGIIVSYAVKVLFLGALGELCAELPFLMHPKPSRKAQL--- 356
QY 361 DSQADVE 367
DB 361 DSQADVE 367
QY 357 EAGSIE 363
DB 357 EAGSIE 363
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RESULT 5

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US-11-097-143-12000
; Sequence 12000, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CLO00728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12000
; LENGTH: 364
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-12000
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Query Match 70.1%; Score 1384; DB 6; Length 364;
Best Local Similarity 70.3%; Pred. No. 9.4e-121;
Matches 258; Conservative 51; Mismatches 54; Indels 4; Gaps 2;

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QY 1 MVAVFYFKKCAPNGKATLYMGKRDVFDHVSQVEPIDIGIVLDDDEYIRDNKRVFGQIVCS 60
DB 1 MVAVFYFKKCAPNGKATLYMGKRDVFDHVSQVEPIDIGIVLDDDEYIRDNKRVFGQIVCS 60
QY 61 FRYGREDEWGLNFGKELCLASQIYPRPEKSKDEQTKQERLLKKLGSNAIPFTFNIS 120
DB 61 FRYGREDEWGLNFGKELCLASQIYPRPEKSKDEQTKQERLLKKLGSNAIPFTFNIS 120
QY 121 PNASSVTLQGGEDDNGDPCGVSYVVKIFAGESETDTHRRSTVTLGIRKIQAPTKOGQ 180
DB 121 PNASSVTLQGGEDDNGDPCGVSYVVKIFAGESETDTHRRSTVTLGIRKIQAPTKOGQ 180
QY 120 PSSPASVTLQGXKSDSQPCGVQYFVKIFGDSDCDRSHRSTINLGIKRVQYAPTKOGI 179
DB 120 PSSPASVTLQGXKSDSQPCGVQYFVKIFGDSDCDRSHRSTINLGIKRVQYAPTKOGI 179
QY 181 QPCTVVRKDFMLSPGSELEVTLDKQLYLHGERIGVNICIRNNSNKKVKKIKAMVQOGVD 240
DB 181 QPCTVVRKDFMLSPGSELEVTLDKQLYLHGERIGVNICIRNNSNKKVKKIKAMVQOGVD 240
QY 180 QPCTVVRKDFMLSPGSELEVTLDKQLYLHGERIGVNICIRNNSNKKVKKIKAMVQOGVD 239
DB 180 QPCTVVRKDFMLSPGSELEVTLDKQLYLHGERIGVNICIRNNSNKKVKKIKAMVQOGVD 239
QY 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOQWYVTLPLSSNKKORGIALLDQIKRODQ 300
DB 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOQWYVTLPLSSNKKORGIALLDQIKRODQ 300
QY 240 VVLFQNGQFRNTIAFMETSEGCPLNPGSSLOQWYVTLPLVANCDBAGIAVEGDIKRKDT 299
DB 240 VVLFQNGQFRNTIAFMETSEGCPLNPGSSLOQWYVTLPLVANCDBAGIAVEGDIKRKDT 299
QY 301 CLASTTLLAOPDQDARGVIIISYAVKVLFLGALGELSAELPVLMPKPKGTAKAYIHA 360
DB 301 CLASTTLLAOPDQDARGVIIISYAVKVLFLGALGELSAELPVLMPKPKGTAKAYIHA 360
QY 300 ALASTTLLASQDARDADFGIIVSYAVKVLFLGALGELCAELPFLMHPKPSRKAQL--- 356
DB 300 ALASTTLLASQDARDADFGIIVSYAVKVLFLGALGELCAELPFLMHPKPSRKAQL--- 356
QY 361 DSQADVE 367
DB 361 DSQADVE 367
QY 357 EAGSIE 363
DB 357 EAGSIE 363
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RESULT 6

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US-10-094-240-25
; Sequence 25, Application US/10094240
; Publication No. US20030082637A1
; GENERAL INFORMATION:
; APPLICANT: ZWIEBEL, LAURENCE J.
; TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF
; FILE REFERENCE: N8289
; CURRENT APPLICATION NUMBER: US/10/094,240
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 10/056,405
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/264,649
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 25
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Anopheles gambiae
US-10-094-240-25
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Query Match 51.8%; Score 1023; DB 4; Length 398;

Best Local Similarity 52.3%; Pred. No. 7.5e-87;
Matches 204; Conservative 65; Mismatches 111; Indels 10; Gaps 7;

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QY 1 MVAVFYFKKCAPNGKATLYMGKRDVFDHVSQVEPIDIGIVLDDDEYIRDNKRVFGQIVCS 60
DB 1 MVAVFYFKKCAPNGKATLYMGKRDVFDHVSQVEPIDIGIVLDDDEYIRDNKRVFGQIVCS 60
QY 61 FRYGREDEWGLNFGKELCLASQIYPRPEKSKDEQTKQERLLKKLGSNAIPFTFNIS 120
DB 61 FRYGREDEWGLNFGKELCLASQIYPRPEKSKDEQTKQERLLKKLGSNAIPFTFNIS 120
QY 121 PNASSVTLQGGEDDNGDPCGVSYVVKIFAGESETDTHRRSTVTLGIRKIQAPTKOGQ 180
DB 121 PNASSVTLQGGEDDNGDPCGVSYVVKIFAGESETDTHRRSTVTLGIRKIQAPTKOGQ 180
QY 119 SMAPSSVTLQAGGEDDNGDPCGVSYVVKIFAGESETDTHRRSTVTLGIRKIQAPTKOGQ 178
DB 119 SMAPSSVTLQAGGEDDNGDPCGVSYVVKIFAGESETDTHRRSTVTLGIRKIQAPTKOGQ 178
QY 181 QPCTVVRKDFMLSPGSELEVTLDKQLYLHGERIGVNICIRNNSNKKVKKIKAMVQOGVD 239
DB 181 QPCTVVRKDFMLSPGSELEVTLDKQLYLHGERIGVNICIRNNSNKKVKKIKAMVQOGVD 239
QY 179 RLPSSLVSKGFTFQOGKINLEVTLDREIYHGEKIANIIVTNSKRTKIVSIKCFVQOHC 238
DB 179 RLPSSLVSKGFTFQOGKINLEVTLDREIYHGEKIANIIVTNSKRTKIVSIKCFVQOHC 238
QY 240 DVVLFQNGSYRNTVASLETSEGCPIQPGSSLOQWYVTLPLSSNKKORGIALLDQIKROD 299
DB 240 DVVLFQNGSYRNTVASLETSEGCPIQPGSSLOQWYVTLPLSSNKKORGIALLDQIKROD 299
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Db 239 EVTMV-NAQFSKHIALETRGCPITPGASFTKSFVLPLASSNKRGRGIALDGHLEKDD 297
Qy 300 QCLASTTLLAOPD-QRPAFVITISYAVKVLFLGALGGEISAEPLFVLMHPKPGT--KAK 356
Db 298 VNLAASSTLISEGKCPDAMGIVISYLRVKLNCCTLGGELQTDVFPFLKMPAPGSVERER 357
Qy 357 VIHADSOADVETFPQDPT---IDQASVDPE 383
Db 358 VNALKKMKSIERRHYENSHYADDDDNITVFE 387

RESULT 7

US-10-954-778-241
; Sequence 241, Application US/10954778
; Publication No. US20050153368A1
; GENERAL INFORMATION:
; APPLICANT: ZWIEBEL, LAURENCE J.
; TITLE OF INVENTION: METHOD OF IDENTIFYING CHEMICAL AGENTS WHICH STIMULATE
; TITLE OF INVENTION: ODORANT RECEPTORS OF SENSORY NEURONS
; FILE REFERENCE: N1125
; CURRENT APPLICATION NUMBER: US/10/954,778
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 10/056,405
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/264,649
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: Patentn Ver. 3.3
; SEQ ID NO 241
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Anopheles gambiae
US-10-954-778-241

Query Match 51.8%; Score 1023; DB 5; Length 398;
Best Local Similarity 52.3%; Pred. No. 7.5e-87;
Matches 204; Conservative 65; Mismatches 111; Indels 10; Gaps 7;

Qy 1 MYVNFKKVCAPKSKVTLVWKGKDPVDHVSQVEPIGIVLDEEYLRDNKRKVGQIVCS 60
Db 1 MYVAVKVFKKSAAPKGLTVLGGKDPIDHDYCPIDGVILDEEYLR-GKRVGQLITTT 59
Qy 61 FRYGREDEWVGLFOKELCLASEQIYPRPEKSDKEQTKLOERLLKLSNAIPFTNIS 120
Db 60 YRIGREDEWVGVFSKEMULTKEQIYPM--ENAMENMPQERLVKLGANAFFFTTHFP 118
Qy 121 PNAPSSVTLQGGEDNDGPGCVSYVVKIFAGESEFTDRTHRSVTTLGIRKIQFAPTKQG 180
Db 119 SMAAPSSVTLQAGEDDTGKPLGVEYAIKAHVGEDESDGKHKSAVTLTIKKLQVAPVSRGR 178
Qy 181 Q-PCTVLRKQFMLSPEGLLEVTLDKQLYLHGERIGVNICIRNNSNMVKKIKAMVQGV 239
Db 179 RLBSVLVSKGTTFQGINLEVTLDREIYHGEKIAIVTNNSRKIVSIRKCFVQHC 238
Qy 240 DVVLFQNGSYRNTVASLETSEGCPIOPGSSLQKVMYVLPPLSSNKKORRGIALDQIKROD 299
Db 239 EVTMV-NAQFSKHIALETRGCPITPGASFTKSFVLPLASSNKRGRGIALDGHLEKDD 297
Qy 300 QCLASTTLLAOPD-QRPAFVITISYAVKVLFLGALGGEISAEPLFVLMHPKPGT--KAK 356
Db 298 VNLAASSTLISEGKCPDAMGIVISYLRVKLNCCTLGGELQTDVFPFLKMPAPGSVERER 357
Qy 357 VIHADSOADVETFPQDPT---IDQASVDPE 383
Db 358 VNALKKMKSIERRHYENSHYADDDDNITVFE 387

RESULT 8

US-11-097-143-1314
; Sequence 1314, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig

; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/167,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1314
; LENGTH: 470
; TYPE: PRT
; ORGANISM: DROSOPHILA

US-11-097-143-1314

Query Match 50.8%; Score 1002; DB 6; Length 470;
Best Local Similarity 53.7%; Pred. No. 9e-85;
Matches 187; Conservative 70; Mismatches 87; Indels 4; Gaps 3;

Qy 6 KVFKKCAPNGKVTLYWKGKDPVDHVSQVEPIGIVLDEEYLRDNKRKVGQIVCSFRYGR 65
Db 48 RVFKSSSNGKIKTVYLGKRFVDHVTVDPIDGVFPIDPEYVD-RKVFQVLAAPFYGR 106
Qy 66 EDEWVGLNFOKELCLASEQIYPRPEKSDKEQTKLOERLLKLSNAIPFTNISPNAPS 125
Db 107 EDDLVLGLTRKQLYLHGEQIYPM--PMQLDPRMTRLOERLLKLSGNAPHYFEVRYCPA 165
Qy 126 SVTLQGGEDNDGPGCVSYVVKIFAGESEFTDRTHRSVTTLGIRKIQFAPTKQGQGPCTL 185
Db 166 SVSLQPARPGVGVSCGVYDLKAFVGENVEDKHKNSVALTIKVMYASSTKVGGEPSIE 225
Qy 186 VRKQFMLSPEGLLEVTLDKQLYLHGERIGVNICIRNNSNMVKKIKAMVQGVVVLFO 245
Db 226 VSKEFMKPKINHLEATLDKELYHNGEKISVNVHVNNSNRYKIKVCVROPADICLFS 285
Qy 246 NGSYRNTVASLETSEGCPIOPGSSLQKVMYVLPPLSSNKKORRGIALDQIKRODCLAST 305
Db 286 TAOYKSVVAIESESDGQVAPGFTLSKVPELCPULANKKQKWLADGQLKHEDTNLASS 345
Qy 306 TLLAOPDQDAFVITISYAVKVLFLGALGGEISAEPLFVLMHPKPGT 351
Db 346 TLTINPAQRESLGMVHYKVKVLLISSPLNGBVLAEPLFTLMHPKPG 393

RESULT 9

US-10-094-240-27
; Sequence 27, Application US/10094240
; Publication No. US20030082637A1
; GENERAL INFORMATION:
; APPLICANT: ZWIEBEL, LAURENCE J.
; TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF
; FILE REFERENCE: N8289
; CURRENT APPLICATION NUMBER: US/10/094,240
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 10/056,405
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/264,649

;; PRIOR FILING DATE: 2001-01-26
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: Patent In Ver. 2.1
;; SEQ ID NO: 27
;; LENGTH: 401
;; TYPE: PRF
;; ORGANISM: Drosophila melanogaster
US-10-094-240-27

Query Match 49.8%; Score 982.5; DB 4; Length 401;
Best Local Similarity 48.7%; Pred. No. 4.8e-83;
Matches 191; Conservative 73; Mismatches 115; Indels 13; Gaps 6;

QY 1 MVNFKYFKKCAPNGKVTLYMGKRDVVDHVGVEPIDGIVLDEYIRDNKRVGQIVCS 60
DB 1 MVNFKYFKKCAPNGKVTLYMGKRDVVDHVGVEPIDGIVLDEYIRDNKRVGQIVCS 59
QY 61 FRYGREDVWGLNFQKELCLASQIYPRPEKSDKEOTKLOERLLKLGSNAPFTFNIS 120
DB 60 FRYGREDVWGLNFQKELCLASQIYPRPEKSDKEOTKLOERLLKLGSNAPFTFNIS 118
QY 121 PNASVTLQOEGDNDGPGCVSYVYKIFAGESETDRTHRSTVTLGIRKIQAPATKQO 180
DB 119 PNASVTLQOEGDNDGPGCVSYVYKIFAGESETDRTHRSTVTLGIRKIQAPATKQO 178
QY 181 Q-PCTLYRKDFMLSPGELAEVTLDKQLYHGERIGVNICIRNNSKNVKKIKAMVOGV 239
DB 179 RLPSSLVSKGFTFSGKISLEVTLDREIYHGEKTAATVQVSNNSKKSXIKCFIVQHT 238
QY 240 DVTLFQNGSYNTVYASLTSBGCPIQPGSSLOKMYLTPLLSSNKGORGIALDQIKROD 299
DB 239 EITWV-NAQFSKHAQOLETEKGCPTTPGANTTKTFYLLPLAANKDRHGIALDGHKDED 297
QY 300 QCLASTTLIAQ-PDQDAFGVLIISYAVKVLFLGALGSELPAELPFVLMHPKPGT----- 353
DB 298 VNLASSTWVGKSTGDAAGIVISYVRIKLNCGTLGEMQTDVDFKLLQAPATIEKKR 357
QY 354 ---KAKVIHADSOADVETFRQDTIDQASVDF 382
DB 358 SNAMKMKMSIEQHNRVKGYYQDDDNIVFEDF 389

RESULT 10
US-11-097-143-12684
;; Sequence 12684, Application US/11097143
;; Publication No. US20050208558A1
;; GENERAL INFORMATION:
;; APPLICANT: Venter, J. Craig
;; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
;; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
;; FILE REFERENCE: CLO00728
;; CURRENT APPLICATION NUMBER: US/11/097,143
;; CURRENT FILING DATE: 2005-04-04
;; PRIOR APPLICATION NUMBER: 60/157,832
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: 60/160,191
;; PRIOR FILING DATE: 1999-10-19
;; PRIOR APPLICATION NUMBER: 60/161,932
;; PRIOR FILING DATE: 1999-10-28
;; PRIOR APPLICATION NUMBER: 60/164,769
;; PRIOR FILING DATE: 1999-11-12
;; PRIOR APPLICATION NUMBER: 60/173,383
;; PRIOR FILING DATE: 1999-12-28
;; PRIOR APPLICATION NUMBER: 60/175,693
;; PRIOR FILING DATE: 2000-01-12
;; PRIOR APPLICATION NUMBER: 60/184,831
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: 60/191,637
;; PRIOR FILING DATE: 2000-03-23
;; NUMBER OF SEQ ID NOS: 43008
;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 12684
;; LENGTH: 401
;; TYPE: PRF
;; ORGANISM: DROSOPHILA
US-11-097-143-12684

Query Match 49.8%; Score 982.5; DB 6; Length 401;
Best Local Similarity 48.7%; Pred. No. 4.8e-83;
Matches 191; Conservative 73; Mismatches 115; Indels 13; Gaps 6;

QY 1 MVNFKYFKKCAPNGKVTLYMGKRDVVDHVGVEPIDGIVLDEYIRDNKRVGQIVCS 60
DB 1 MVNFKYFKKCAPNGKVTLYMGKRDVVDHVGVEPIDGIVLDEYIRDNKRVGQIVCS 59
QY 61 FRYGREDVWGLNFQKELCLASQIYPRPEKSDKEOTKLOERLLKLGSNAPFTFNIS 120
DB 60 FRYGREDVWGLNFQKELCLASQIYPRPEKSDKEOTKLOERLLKLGSNAPFTFNIS 118
QY 121 PNASVTLQOEGDNDGPGCVSYVYKIFAGESETDRTHRSTVTLGIRKIQAPATKQO 180
DB 119 PNASVTLQOEGDNDGPGCVSYVYKIFAGESETDRTHRSTVTLGIRKIQAPATKQO 178
QY 181 Q-PCTLYRKDFMLSPGELAEVTLDKQLYHGERIGVNICIRNNSKNVKKIKAMVOGV 239
DB 179 RLPSSLVSKGFTFSGKISLEVTLDREIYHGEKTAATVQVSNNSKKSXIKCFIVQHT 238
QY 240 DVTLFQNGSYNTVYASLTSBGCPIQPGSSLOKMYLTPLLSSNKGORGIALDQIKROD 299
DB 239 EITWV-NAQFSKHAQOLETEKGCPTTPGANTTKTFYLLPLAANKDRHGIALDGHKDED 297
QY 300 QCLASTTLIAQ-PDQDAFGVLIISYAVKVLFLGALGSELPAELPFVLMHPKPGT----- 353
DB 298 VNLASSTWVGKSTGDAAGIVISYVRIKLNCGTLGEMQTDVDFKLLQAPATIEKKR 357
QY 354 ---KAKVIHADSOADVETFRQDTIDQASVDF 382
DB 358 SNAMKMKMSIEQHNRVKGYYQDDDNIVFEDF 389

RESULT 11
US-09-880-137-3
;; Sequence 3, Application US/09880137
;; Patent No. US20020031295A1
;; GENERAL INFORMATION:
;; APPLICANT: Berstein, Gabriel
;; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
;; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
;; FILE REFERENCE: MNI-131
;; CURRENT APPLICATION NUMBER: US/09/880,137
;; CURRENT FILING DATE: 2001-03-05
;; PRIOR APPLICATION NUMBER: US 60/186,706
;; PRIOR FILING DATE: 2000-03-03
;; NUMBER OF SEQ ID NOS: 8
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 3
;; LENGTH: 410
;; TYPE: PRF
;; ORGANISM: Homo sapiens
US-09-880-137-3

Query Match 46.0%; Score 907.5; DB 3; Length 410;
Best Local Similarity 47.2%; Pred. No. 5.3e-76;
Matches 176; Conservative 78; Mismatches 112; Indels 7; Gaps 4;

QY 6 KVFKKCAPNGKVTLYMGKRDVVDHVGVEPIDGIVLDEYIRDNKRVGQIVCSFRYGR 65
DB 7 RVFKKASPNKLTLYVYGRDVFVDHIDVDPDGVVLDVPEYLKE-RRVYVTLTCAFRRGR 65
QY 66 EDEVMGYNFQKELCLASQIYPRPEKSDKEOTKLOERLLKLGSNAPFTFNISPNAPS 125
DB 66 EDLVDVLTGLTFRKDLFVANVQSFPPAPEDKKLTIRQERLLKLGSHAYPFTFELPNLPC 125
QY 126 SVTLQOEGDNDGPGCVSYVYKIFAGESETDRTHRSTVTLGIRKIQAPATKQOQOQCTL 185

Db	126	SVTLDPGDEDTKACGVDEYVAFCAENIEEKIKHNSVRLYIRKQVAPRRGPOPTAE	185
Qy	186	VRKDFMISGGELELEVTLDKOLYLHGERIGVNI CIRNNSNKKVKKIKAMYOQGVDDVLFQ	245
Db	186	TTROFLMSDKPRLHLEASLDKEIYYHGEPISVNVVHTNNNTKVKIKIISVROYADICLPN	245
Qy	246	NGSYNNTVAASLETSEGCPIQOPSSLOKWYLTPLLSNKKORGIALDGOIKRODOCLAST	305
Db	246	TAQYKCPVAMEBAD--TVAPSTFECKVYTLPLPLANNREKGLADGKLKHEDTVLASS	303
Qy	306	TLIAQPDORDACGVISVAVKYKTLPLGALGELSELPLVLMHPKRGTK--AKYVHAS	362
Db	304	TLIRGGANNEIGILVSYKYVKYL-VESKGVDAVELPPTLMAHFKXEPRRHREVENET	362
Qy	363	QADVETFRQDITD	375
Db	363	PVDNTLIELDTND	375

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RESULT 12
US-09-800-137A-3
Sequence 3, Application US/09800137A
Publication No. US20030157553A1
GENERAL INFORMATION:
APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
FILE REFERENCE: MN1-131
CURRENT APPLICATION NUMBER: US/09/800,137A
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/166,706
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PasteSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 410
TYPE: PRT
ORGANISM: Homo sapiens
US-09-800-137A-3

```

Query Match	46.0%	Score 907.5;	DB 3;	Length 410;
Best Local Similarity	47.2%	Pred. No. 5.3e-76;		
Matches 176;	Conservative 78;	Mismatches 112;	Indels 7;	Gaps 4

```

Qy 6 VYEFKCAPIRGKTYLWKGXDVPVDHNSGVBRIGIVLDBEYUJRDNKKRGVQJICSPRYGR 65
Db 7 RVFKASPIRGKTYLVGKGRDVPVDHIDLVPDGVVLVDEPLYE--RRVYUJTLCAFRYGR 65
Qy 66 EDEWVGINTFOKELCLASBOIYRPERKSDKEOQKLOERLLKLGSAIAPFTFNISFNAS 125
Db 66 EDLDVIGLTFKRDLPVANYQSFPRAPEDKKPLTRLOERLLKLGSAIAPFTFEIPNNLPC 125
Qy 126 SVTLTQQGEDNDGPGCVSYVYKIFAGESEBTRTHRSSTVLTGIRKIQAPATKGGQOPCTL 185
Db 126 SVTLTQGPREDTQKACGVDEYVAKFAEINTEBEKIHKNSVRLVIRKQVAPREBGPQTAE 185
Qy 186 VRKDMLSBGELEEVTLDKOLYHNERGVNICINNSNKWYKIKIKAWYQGVDPVVLFPQ 245
Db 186 TTRQELMSDKRPHLEASLDKEIYYHGEPISVNHNVTNNNTKIVKIKIISVROYADICLEN 245
Qy 246 NGSYNTVYASLETSEGCPIQPGSSLOKWMYLPFLSSNKORRGIALDGOIKRPODCLAST 305
Db 246 TAQYICCPVAMEADDD--TVAPSSTFCKYVTLTLPFLANNEEKGALDQKIKHEDTDLASS 303
Qy 306 TLLAOPDORDAFVGIISYAVKYKLPGLAGELGISAELPVLNMPKPGTK--AKVTHADS 362
Db 304 TLLREGANREILGIIYSYKVKYKL--VESRGGDVAVELPFLNMPKPREBPRHREVENET 362
Qy 363 QADVETPRODTID 375
Db 363 PVDTNLIELDTND 375

```

```

RESULT 13
US-09-880-137-1
; Sequence 1, Application US/09880137
; Patent No. US20020011295A1
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: MN-111
; CURRENT APPLICATION NUMBER: US/09/880.137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-880-137-1

```

Query Match	Similarity	45.8%	Score 903.5	DB 3	Length 418
Best Local	Similarity	47.1%	Pred. No. 1.3e-75		
Matches	179	Conservative	76	Mismatches	112
				Indels	13
				Gaps	5
QY	6	KVFKKCAENGKVTLLYMGKRDPVDHVSQVEPIDGIYVLDDDEXIRDNKVKQGVCSFRYGR	65		
		: : : : : : : : : : : : : :			
DB	7	RVFKKASPNGLTLYLIGKRDPVDHIDLVEPYDGVVLVDPEYLK-RRVYVLTLCAFRYGR	65		
QY	66	FEDFVMGAINFOKELCLASBQIYPRPEKSDKQOTLOEFLIKKLSGNAIPFENTSPNBS	125		
		: : : : : : : : : : : : : :			
DB	66	EDLVNLGLTFKRDLFVANVQSFPPAPEKKPLTRLOEKLKLGNAHPFELPPLNPLC	125		
QY	126	SVTLLOQGEDNDGDCQGSYYVVKIFAGESBETRTRASTYLTGIRKIOEAPTRKQGOQPC	185		
		: : : : : : : : : : : : : :			
DB	126	SVTLLOQGEDNDGCKAGVDYEVKAFCAENLEBKIHKRNSTRVLIRKVVQYAPRBPQPAE	185		
QY	186	VKRDPMLSFGELELEFVTLDKOLYLHGEFIGNVICTRNNSNKKVKKIKMYMOQGVVLV	245		
		: : : : : : : : : : : : : :			
DB	186	TTRPFLMSDKPLHEASLDKEIYYHGERISVNVHTVNTNTKTVKKIKISVQYADICFN	245		
QY	246	NGSVRNTVASLETSGECPRIQPGSSLOKMYLTPLLSSKORGLALDQIKRODOCLAST	305		
		: : : : : : : : : : : : : :			
DB	246	TAQYKCPALMEABD--TVAPSSFTCKYTLTLPFLANNREKGLALDKLKHEDNTNLSS	303		
QY	306	TLLAQPDORDAFGVIISAYVKKVFL--GALGGBLSA-----ELPVLMMHPKGTK--A	355		
		: : : : : : : : : : : : : :			
DB	304	TLLREGANREILIGIIVSYKVKVLVSSGGLGLDGLASSDVALEPFLTMHPKPEEPHR	363		
QY	356	KVIHADSOADYVTRQDPTID 375			
		: : : : : : : : : : : : : :			
DB	364	EVPEHETPVDTNLIELDTND 383			

```

RESULT 14
US-09-800-137A-1
Sequence 1, Application US/098000137A
Publication No. US2003015755A1
GENERAL INFORMATION:
APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
FILE REFERENCE: NMI-131
CURRENT APPLICATION NUMBER: US/09/800,137A
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/166, 706
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 418
TYPE: BRT

```

ORGANISM: Bos taurus
US-09-800-137A-1

Query Match 45.8%; Score 903.5; DB 3; Length 418;
Best Local Similarity 47.1%; Pred. No. 1.3e-75;
Matches 179; Conservative 76; Mismatches 112; Indels 13; Gaps 5;

QY 6 KVFKKCAPNGKVTLYMGKRDVFDHVSVEPIIDGIVLDDDEYIRDNKRYFGQIVCSFRYGR 65
DB 7 RVFKKASPNKGLTYVLGKRDFVDHIDIVEPVDGVLDPEYLAKE-RRVYVTLTCAFRYGR 65
QY 66 EDEVMGNIPOKELCLASEQIYPRPEKSDKEQTLQOEELKKLSNAPFFENISPNAPS 125
DB 66 EDLDVLGTFRRKDLFVANVQSPAPAPEDKKPLTRQERLTKLGBHAIPFFELPPNIPC 125
QY 126 SVTLQOGEDNDGDCGVSYYVKIFAGESEFDRTRHRSSTVTLGIRKIQAPPTKQGOQPC 185
DB 126 SVTLQOPEPDTGKACGVYEVKAFCAENLEBKIHKNSVRLVIRKQYAPERPQPTAE 185
QY 186 VRKDFMLSPGELELVTLDKQLYLHGERIGVNICIRNNSKMYKKIKAMVQGVVDVLFQ 245
DB 186 TTRQFLMSDKPLHLSEASLDKEIYYHGEPISVNVHTNTNTKTVKKIKISVRQYADICLFN 245
QY 246 NGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLLSNKORRGIALDGOIKRODQCLAST 305
DB 246 TAQYKCPVAMEEADD--TVAPSSTFCKVYTLTPFLANNREKGLALDGKXKHEDTNLASS 303
QY 306 TLLAOPDQDAFGVYISYAVKVLFL--GALGELSA-----ELPVLAMHPKPGTK--A 355
DB 304 TLLREGANREILGIVSYKVKVLYVSRGGLGDASSDVAVELPFTLMHPKPKKEPPHR 363
QY 356 KVIHADSOADVETFRQDTID 375
DB 364 EVPEHETPVDTNLIELDTND 383

RESULT 15
US-10-038-010-52
; Sequence 52, Application US/10038010
; Publication No. US20030040089A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; APPLICANT: Pierre, Legrain
; TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
; FILE REFERENCE: B4767A
; CURRENT APPLICATION NUMBER: US/10/038,010
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 60/259,377
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patent version 3.1
; SEQ ID NO 52
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: beta Arrestin 1
; LOCATION: (1)..(452)
; OTHER INFORMATION:
US-10-038-010-52

Query Match 45.8%; Score 903.5; DB 4; Length 452;
Best Local Similarity 47.1%; Pred. No. 1.5e-75;
Matches 179; Conservative 76; Mismatches 112; Indels 13; Gaps 5;

QY 6 KVFKKCAPNGKVTLYMGKRDVFDHVSVEPIIDGIVLDDDEYIRDNKRYFGQIVCSFRYGR 65
DB 7 RVFKKASPNKGLTYVLGKRDFVDHIDIVEPVDGVLDPEYLAKE-RRVYVTLTCAFRYGR 65
QY 66 EDEVMGNIPOKELCLASEQIYPRPEKSDKEQTLQOEELKKLSNAPFFENISPNAPS 125
DB 66 EDLDVLGTFRRKDLFVANVQSPAPAPEDKKPLTRQERLTKLGBHAIPFFELPPNIPC 125

QY 126 SVTLQOGEDNDGDCGVSYYVKIFAGESEFDRTRHRSSTVTLGIRKIQAPPTKQGOQPC 185
DB 126 SVTLQOPEPDTGKACGVYEVKAFCAENLEBKIHKNSVRLVIRKQYAPERPQPTAE 185
QY 186 VRKDFMLSPGELELVTLDKQLYLHGERIGVNICIRNNSKMYKKIKAMVQGVVDVLFQ 245
DB 186 TTRQFLMSDKPLHLSEASLDKEIYYHGEPISVNVHTNTNTKTVKKIKISVRQYADICLFN 245
QY 246 NGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLLSNKORRGIALDGOIKRODQCLAST 305
DB 246 TAQYKCPVAMEEADD--TVAPSSTFCKVYTLTPFLANNREKGLALDGKXKHEDTNLASS 303
QY 306 TLLAOPDQDAFGVYISYAVKVLFL--GALGELSA-----ELPVLAMHPKPGTK--A 355
DB 304 TLLREGANREILGIVSYKVKVLYVSRGGLGDASSDVAVELPFTLMHPKPKKEPPHR 363
QY 356 KVIHADSOADVETFRQDTID 375
DB 364 EVPEHETPVDTNLIELDTND 383

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74.376 Million cell updates/sec

Title: US-10-056-405-2

Perfect score: 1 MVNFKYKKCAPNGKVTLY.....ADVFTRQDTIIDQASVDFE 363

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 21570 seqs, 2136119 residues

Total number of hits satisfying chosen parameters: 21570

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA New:*

- 1: /EMC_CeJelerra_SIDS3/ptodata/2/pubppaa/US09_NEW_PUB.pep:*
- 2: /EMC_CeJelerra_SIDS3/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
- 3: /EMC_CeJelerra_SIDS3/ptodata/2/pubppaa/US07_NEW_PUB.pep:*
- 4: /EMC_CeJelerra_SIDS3/ptodata/2/pubppaa/US08_NEW_PUB.pep:*
- 5: /EMC_CeJelerra_SIDS3/ptodata/2/pubppaa/PC7_NEW_PUB.pep:*
- 6: /EMC_CeJelerra_SIDS3/ptodata/2/pubppaa/US10_NEW_PUB.pep:*
- 7: /EMC_CeJelerra_SIDS3/ptodata/2/pubppaa/US11_NEW_PUB.pep:*
- 8: /EMC_CeJelerra_SIDS3/ptodata/2/pubppaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	885	44.9	409	US-10-505-928-173	Sequence 173, App
2	81.5	4.1	862	US-10-511-937-2374	Sequence 2374, App
3	80	4.1	800	US-10-196-749-478	Sequence 478, App
4	77.5	3.9	1212	US-10-505-928-201	Sequence 201, App
5	77	3.9	282	US-11-251-466-46	Sequence 46, App
6	77	3.9	282	US-11-264-784-72	Sequence 72, App
7	75.5	3.8	893	US-10-505-928-733	Sequence 733, App
8	74.5	3.8	299	US-10-196-749-164	Sequence 164, App
9	74.5	3.8	708	US-11-170-482-16	Sequence 16, App
10	73	3.7	763	US-10-505-928-324	Sequence 304, App
11	72.5	3.7	806	US-11-251-465-22	Sequence 22, App
12	72.5	3.7	1075	US-10-322-838-48	Sequence 48, App
13	72.5	3.7	2215	US-10-505-928-310	Sequence 310, App
14	71	3.6	798	US-10-511-937-2451	Sequence 2451, App
15	71	3.6	871	US-11-316-132-1	Sequence 1, App
16	71	3.6	3113	US-10-505-928-325	Sequence 325, App
17	70.5	3.6	1809	US-10-559-415-190	Sequence 190, App
18	70.5	3.6	1919	US-10-559-415-2	Sequence 2, App
19	70	3.5	301	US-11-101-316-18	Sequence 18, App
20	69	3.5	870	US-11-316-132-2	Sequence 2, App
21	68.5	3.5	709	US-11-170-482-14	Sequence 14, App
22	67.5	3.4	318	US-11-106-014-42	Sequence 42, App
23	67.5	3.4	729	US-11-312-958-64	Sequence 64, App
24	67.5	3.4	1443	US-10-505-928-720	Sequence 720, App
25	67	3.4	725	US-10-370-959-128	Sequence 128, App

26	67	3.4	725	6	US-10-370-959-135	Sequence 135, App
27	67	3.4	1189	7	US-11-311-778-20	Sequence 20, App
28	67	3.4	1395	6	US-10-505-928-513	Sequence 513, App
29	66.5	3.4	184	7	US-11-327-800-8	Sequence 8, App
30	66.5	3.4	432	6	US-10-505-928-363	Sequence 363, App
31	66.5	3.4	919	7	US-11-251-465-31	Sequence 31, App
32	66.5	3.4	1215	6	US-10-505-928-75	Sequence 75, App
33	66.5	3.4	1539	6	US-10-511-937-2545	Sequence 2545, App
34	66	3.3	298	6	US-10-322-836-50	Sequence 50, App
35	66	3.3	695	7	US-11-170-482-18	Sequence 18, App
36	66	3.3	993	6	US-10-511-937-2463	Sequence 2463, App
37	66	3.3	3256	6	US-10-505-928-357	Sequence 357, App
38	65.5	3.3	246	7	US-11-249-111-123	Sequence 123, App
39	65.5	3.3	343	6	US-10-478-743B-4	Sequence 4, App
40	65.5	3.3	642	7	US-10-505-928-259	Sequence 259, App
41	65.5	3.3	653	7	US-11-183-218-66	Sequence 66, App
42	65.5	3.3	851	6	US-10-511-937-2597	Sequence 2597, App
43	65.5	3.3	1333	6	US-10-511-937-2992	Sequence 2992, App
44	65.5	3.3	2351	7	US-11-183-218-30	Sequence 30, App
45	65.5	3.3	2351	7	US-11-280-757-35	Sequence 35, App

ALIGNMENTS

RESULT 1
US-10-505-928-173
; Sequence 173, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research
; TITLE OR INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; PRIOR FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 173
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-173

Query Match 44.9%; Score 885; DB 6; Length 409;
Best Local Similarity 48.3%; Pred. No. 1.5e-90;
Matches 167; Conservative 77; Mismatches 98; Indels 4; Gaps 3;

QY	6	KVFKKCAPNGKVTLYMGKRDVDHVGVEPTDGI:VVLDDDEXIRDNKRVFGQIVCSFRYGR	65
DB	8	RVFKKSSPNCKLTVYLGKRDVDHLDKVDVGVVLDVDPDLKO-RKVFVTLTCAFRYGR	66
QY	66	EEDVMGILFQKELCLASEQIYPRPEKSDKQTKLOERLKKLSNMIPTFNISPNAPS	125
DB	67	EDDLVLGSPFKDIFIAFYQAFPPVPNPPRPRTLQORLRLKQGHAFPTTIPQNLPC	126
QY	126	SVTLQGGEDNDGDCGVSYVYKIFAGSESDTRTRRSTVTYLGIRKIOPAPTKGQOQPTL	185
DB	127	SVTLQGGEDNDGKAGVDFEIRAFCAKSLBKSHKRNVSRLVIRKVOFAPAPKPGQPSAE	186
QY	186	VKQPMLSRGLLELVTLDKOLYLHGERIGVNICIRNNNSNMGVKKIKMVOGVVVLV	245
DB	187	TRRHFLLMSDRSLHLASDIDKELYHGEPLVNVHVNNTSTTVKKIKVSVQYADICFS	246
QY	246	NGSYRNTVASLETSBGCPIDPGSSLOKVMYTLPLSSNKKORGLALDQIKRQDQCLAST	305
DB	247	TAQKCPVAQLEQDD--QVSPSSTFCKVYTTITPLSDRREKRGALDQKLHEDTNLASS	304
QY	306	TLLAQPDGRDAFGVITISAVVYKFLGALGELSAELPFVLMHRKP	351
DB	305	TIVGANKREVILGISYRVKVLVV-SRGDGVSELPFVLMHRKP	349

```
RESULT 2
US-10-511-937-2974
; Sequence 2974, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Mohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 50661200104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2974
; LENGTH: 862
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2974

Query Match      4.1%; Score 81.5; DB 6; Length 862;
Best Local Similarity 20.6%; Pred. No. 1;
Matches 60; Conservative 51; Mismatches 129; Indels 51; Gaps 13;

QY 22 GKRDFVHVSQVEPIDGIVLDEY---IRDNKRVFQIVCSPPRGREEDVGLN--- 74
DB 525 GDRSQGHVSQELAP---ETDDBSFSDVDCSHNOEDTG---CKFRVLBPQPNLAPTPITKR 578
QY 75 FQKELCLASEQIYPRPEKSKDEQTKLQERLLKLGSAIIPFTFNISPNAPSSVTL-QQGE 133
DB 579 FKKEILLSSSDICQKLVNT-QDMSASQVDAVAVINKKVVPLDFSMSSIAKRIKOLHHAQ 637
QY 134 DNDGDPGCVSYVVIIFAGESEDTKTRHRSYV-----LGIRKIQFATKQGG----- 180
DB 638 QSEGEQYRRKRAKICPENQAEDELRKEISKTMFAEMELIIGQFNIGFIITKLNEDIPI 697
QY 181 --QPCITVRKDFMSPGELLEVTLDKQLYLHGERI---GVNICIRNNSNMKWKIKAM 234
DB 698 VDHQATBEKNFEM-----LQCHTVLQGGRLNAPOTLNLTAVNEA-VLENLLEIF 746
QY 235 VQGGVDVLFQNG--SYRNTVASLETSEGCPIQPGSSLOQVMVLTPLLISSN 283
DB 747 RKNQFDEVIDENAPVTERAKLISLPTSKMTFGP-----QDVDELIFMLSDS 793

RESULT 3
US-10-196-749-478
; Sequence 478, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Uian
; APPLICANT: Deenoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
```

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APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACTDS ENCODING THE SAME
; FILE REFERENCE: P9430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 478
; LENGTH: 800
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-196-749-478

Query Match      4.1%; Score 80; DB 6; Length 800;
Best Local Similarity 19.6%; Pred. No. 1.3;
Matches 94; Conservative 69; Mismatches 167; Indels 150; Gaps 25;

QY 9 KKCAPNGKVTLY-----MGRDFVHVSQVEPIDGIVLDEYIRDRKV 53
DB 94 KLCGPKRPMCLYPIFLMDDPFQIYRAELRYRDINDHAPVQDKETVYKISENTAEGT--- 150
QY 54 FQGIQVCSFRYGREDEVGLN-----FQKELCLASE-QIYPR---PEKSDKEQ 97
DB 151 -----AFRLERADPDGGLNGIQNTYIISPNSFFHINISGDEGMIVPELVLDKALDREE 204
QY 98 -----TYLQERLLKLGSAIIP--TFNISPNAPS-SVTLQGEEDNDGDPGCVSYVVK 147
DB 205 QGELSLTLTLALDGGSPERSGSTVRIVLDVNDAPQFQALYETQAPENSPIGF-LIVK 263
QY 148 IFAGESEDTKTRHRSYVTLGIRKIQFAPTKQGGQPCITLVRKDFMLSP--GELLEVTLDK 205
DB 264 VMAEDVD-----SGNAEVSYSFFDASEN-----ITTPQINFSGEILFRELDDY 309
QY 206 QLYIAGERIGVNICIRNNSNMKWKIKAMVQGGVDV-----VLQON-----GSYR 250
DB 310 ELV-----NSYKI--NIQAMDGGGGSARCVLVEVLDTNPNPELIVSSFS 353
QY 251 NTVASLETSEGCP-----QPGSSLOQVMVLT-----LSSNKQRGI-----ALDG 293
DB 354 NSVA--ENSPETPAVFKINDRDSGENGMKVCYIQENLPLFKKSVENFYLITLREGALDR 411
QY 294 QIKRQDCLASTLLAOPDQDAFGVIT-----SYAVKVK-----LFLG 332
DB 412 EIRAEVNTITVTDLGTPRLKTEINIVLVSDVDNAPAFQTQISYTLFVRENNPALHIG 471
QY 333 ALGGE-----LSAEPLVLMHPK---PGTKAKYIHADSQADVETFPQDITDQASVDFE 383
DB 472 SVSATDRDSGTNAQVTSLLPQPDPHPLASLIVSINADNG---HLFALRSIDYBALQAFE 528

RESULT 4
US-10-505-928-201
```


Sequence 201, Application US/10505928
Publication No. US20060088532A1
GENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research et al.
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: PatentIn 3.2
SEQ ID NO 201
LENGTH: 1212
TYPE: PRT
ORGANISM: Homo sapiens
US-10-505-928-201

Query Match 3.9%; Score 77.5; DB 6; Length 1212;

Best Local Similarity 20.8%; Pred. No. 5.2; Matches 74; Conservative 50; Mismatches 152; Indels 79; Gaps 17;

QY 56 QIVCSFRGRRE-DEVMGLNFQKELCLASEQIYPRPEKSDKQOTLQORLLKLGSMNIP 114
DB 404 QIKQEFRRGTSLDHLAAGLSHYH-ADTSYRHFPSKESKISRLTLEQAKQLPA-ALL 461
QY 115 FTFN-----ISPNAFSSVTLQOGEDNDGDCGVSYV---KIFAGESETDTRHRS 163
DB 462 YQKSKHKKSLIDPMKSKFSPQESRDLEPD---YSSWTSTSSIGISSARL-LQDD 517
QY 164 VTLGRK-----IQPAPFKQOQOPCTL---VRKDMLSFGELEVTLDKQLYHGER-- 213
DB 518 ITFGIRKNTDQOKFMGSSLGTLGTLGNTIRS-----ALODEADKP-YSSGSSSR 567
QY 214 -----IGNVICRNNNNKMKVKKIKAMVOGVVVLFFONGSYNTVASLETS-EGCPI 264
DB 568 PSSRSSSYGLDLSTKRSSSSSLRLKQOEALV-----SFHASSSARTKTSLP 621
QY 265 QPGSSLOKMYLTPLLSSNNKQRG-IALDQIKRODOCLASTTLAOPDQDAFGVITISY 323
DB 622 SQSRG-----RIPVANOSEESPLSPVQGMGMAAAGLPISADTRDQFG----- 670
QY 324 AVKVKLFLGALGELSAELPFVLMHPKGTAKVTHASQADVEFRDPTIDQQA 378
DB 671 -----SSHSLPEVQOQHMBESRTGRGYDRDIATMDFOHAMSSEA 711

RESULT 5

US-11-251-466-46

Sequence 46, Application US/11251466

Publication No. US20060094090A1

GENERAL INFORMATION:

APPLICANT: E.I. duPont de Nemours and Company

APPLICANT: Xue, Zhixiong

TITLE OF INVENTION: A MORTIERELLA ALPINA LYSOPHOSPHATIDIC ACID ACUTRANSFERASE

TITLE OF INVENTION: HOMOLOG FOR ALTERATION OF POLYUNSATURATED FATTY ACIDS AND OIL

TITLE OF INVENTION: CONTENT IN OLEAGINOUS ORGANISMS

FILE REFERENCE: C12793 USNA

CURRENT APPLICATION NUMBER: US/11/251,466

CURRENT FILING DATE: 2005-10-14

PRIOR APPLICATION NUMBER: US 60/624812

PRIOR FILING DATE: 2004-11-04

NUMBER OF SEQ ID NOS: 55

SOFTWARE: PatentIn version 3.3

SEQ ID NO 46

LENGTH: 282

TYPE: PRT

ORGANISM: Yarrowia lipolytica

US-11-251-466-46

Query Match 3.9%; Score 77; DB 7; Length 282;

Best Local Similarity 24.8%; Pred. No. 0.49;

Matches 58; Conservative 29; Mismatches 77; Indels 70; Gaps 14;
QY 144 YVVKIFAGESETDTRHRSVTLGI--RKIOFAP-----TKQGOQCTLVKDKMPLS 193
DB 53 YSVRIFLGISIKLRS-RQVGTAGLDASKIQVANTTKPIDITGHLPRPCLISN---H 107
QY 194 PGELEL-----EVLTDKQLY---LHGERIGVNICI---RNNNNKVVKKIKAMVQ 236
DB 108 QNEMDILVLRIFPQYCSVTAKKALKMYPLLGQFMALSGTIFLDRKORTSVQTLGAVK 167
QY 237 -----QGVVVVLFONG--SYRNTVASLETSEGC---PIQPGSSLOKMYLTPLLSSN 283
DB 168 TIQSGNGKQGSVMPFEGRTSYSKDVGINPFKKGCFHLAVQSGAP-----IYVVVQON 221
QY 284 KOR-----RGIALDQI-----KRQD-----QCLASTTLAOPDQDAFG 318
DB 222 TSRMFSFGKLDAGEILVLDVLSPIETKGLDASNVDALMATTYKACETADQIG 275

RESULT 6

US-11-264-784-72

Sequence 72, Application US/11264784

Publication No. US20060094092A1

GENERAL INFORMATION:

APPLICANT: E.I. duPont de Nemours & Co., Inc.

APPLICANT: Damude, Howard Glenn

APPLICANT: Gillies, Peter John

APPLICANT: Maccoi, Daniel Joseph

APPLICANT: Picatagallo, Stephen K.

APPLICANT: Pollak, Dana M. Walters

APPLICANT: Ragghianti, James John

APPLICANT: Xue, Zhixiong

APPLICANT: Yadav, Narendra S.

APPLICANT: Zhang, Hongxiang

TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA

FILE REFERENCE: C13136 USNA

CURRENT APPLICATION NUMBER: US/11/264,784

CURRENT FILING DATE: 2005-11-01

NUMBER OF SEQ ID NOS: 375

SOFTWARE: PatentIn version 3.3

SEQ ID NO 72

LENGTH: 282

TYPE: PRT

ORGANISM: Yarrowia lipolytica

US-11-264-784-72

Query Match 3.9%; Score 77; DB 7; Length 282;

Best Local Similarity 24.8%; Pred. No. 0.49; Matches 58; Conservative 29; Mismatches 77; Indels 70; Gaps 14;

QY 144 YVVKIFAGESETDTRHRSVTLGI--RKIOFAP-----TKQGOQCTLVKDKMPLS 193
DB 53 YSVRIFLGISIKLRS-RQVGTAGLDASKIQVANTTKPIDITGHLPRPCLISN---H 107
QY 194 PGELEL-----EVLTDKQLY---LHGERIGVNICI---RNNNNKVVKKIKAMVQ 236
DB 108 QNEMDILVLRIFPQYCSVTAKKALKMYPLLGQFMALSGTIFLDRKORTSVQTLGAVK 167
QY 237 -----QGVVVVLFONG--SYRNTVASLETSEGC---PIQPGSSLOKMYLTPLLSSN 283
DB 168 TIQSGNGKQGSVMPFEGRTSYSKDVGINPFKKGCFHLAVQSGAP-----IYVVVQON 221
QY 284 KOR-----RGIALDQI-----KRQD-----QCLASTTLAOPDQDAFG 318
DB 222 TSRMFSFGKLDAGEILVLDVLSPIETKGLDASNVDALMATTYKACETADQIG 275

RESULT 7

US-10-505-928-733

Sequence 733, Application US/10505928

Publication No. US20060088532A1

GENERAL INFORMATION:

```

; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; PRIOR FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 733
; LENGTH: 893
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-505-928-733

Query Match      3.8%; Score 75.5; DB 6; Length 893;
Best Local Similarity 19.7%; Pred. No. 5.1;
Matches 95; Conservative 64; Mismatches 155; Indels 169; Gaps 22;

QY 19 LYMGRPFVD--HYSGVEPIDGIVLDE--YIRDNRKVFQGVCSFRYGEDEWGLN 74
DB 358 LIRGLELYVSARKYVEVERKATPLDENEGIVVDVTKGRAVIGSTYMLTDEVL--- 414
QY 75 FOKELCLASEQIY-----PREPKSKQTKLQERLLKKGSMALPTFNISPNAPSSVTL 129
DB 415 WEKELPFGVEELINKGQDPLADRGKDTAK-----SLQPLAPRNKTR 456
QY 130 QQSGDDNDGPGCVSYVYKIFAGESETDRTNRSTVTIGIKRIQAPRTKQ-----G 179
DB 457 V-----VSRYVPHNNAVQVYDREKRRARVVGPELVSLGPEEQFTVLSLAGRP 505
QY 180 QQP-----CTLYVKRDFMLSPGELELVTLDKOLYHGERIGVNICIRNNSENK----- 226
DB 506 KRPIARRALCLLLRPDFTD--VTITIEDHARQLQ---QLAYWHNEVNRKRPQETAK 560
QY 227 -----MWKKIKAMVQGVVULF---QNGS--YRNTVASLETSEG----- 261
DB 561 LFSVPDFVGACKALIASRVGAVASVTFDDFNKNSARIIRTAIVFGFETSEAKGPDGMALP 620
QY 262 -----CPIQP-----GSSIQKVMYVLPPLSSNKQRGIMLD----- 292
DB 621 RPRDQAVFPONGLVSSVVDVQSVDRDRTDALQRSVQLAIEITTSQDEAAKHQRL 680
QY 293 -----GQIKRQ---DQCLA-----STTLAQPDQR-----DAFGV 319
DB 681 EQEAKGRLERKIIDQSEAEKAKLELEALSMAVESTGTAKEAEERAAARIEGGS 740
QY 320 IISYAVKVKLFLGALGSELNLPV-----LMPKPGTKARVIAHDSQADVET--FR 370
DB 741 VL-----QAKLKQAQLAITEAEALQVQKVRLELVVYARAQLEHVSRAQQLAEVVKFK 796
QY 371 QDT 373
DB 797 QMT 799

RESULT 8
US-10-196-749-164
; Sequence 164, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
```

```

; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 164
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-196-749-164

Query Match      3.8%; Score 74.5; DB 6; Length 299;
Best Local Similarity 26.2%; Pred. No. 1;
Matches 32; Conservative 21; Mismatches 44; Indels 25; Gaps 6;

QY 63 YGREDEWGLNFQKELCLASEQIYPRPKS-----DKQTKQERLLKKGSN--- 111
DB 44 FGTEEBI-----QECIEFTLRLYTRKKPNYELLEKEVEKRVLAQEAFLKKGKLPDG 97
QY 112 --AIPFTFNISP-NAPSSVTLQCGEDNDGPGCVSYVYKIFAESEEDRTHRSSTVTLGI 168
DB 98 TPAISTLGFGFSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSP 152
QY 169 RK 170
DB 153 RK 154

RESULT 9
US-11-170-482-16
; Sequence 16, Application US/11170482
; Publication No. US20060094037A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Paul E.
; APPLICANT: University of Toronto
; TITLE OF INVENTION: PROTEINS RELATED TO SCHIZOPHRENIA AND USES THEREOF
; FILE REFERENCE: 1034/1H570
; CURRENT APPLICATION NUMBER: US/11/170,482
; PRIOR FILING DATE: 2005-06-28
; PRIOR APPLICATION NUMBER: US/09/945,258
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,889
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 708
; TYPE: PRT
; ORGANISM: mouse
; US-11-170-482-16
```

Query Match 3.8%; Score 74.5; DB 7; Length 708;
Best Local Similarity 19.3%; Pred. No. 4.4;
Matches 59; Conservative 44; Mismatches 102; Indels 101; Gaps 14;

QY 6 KVFKK-----ANGKTYL-MGRDVFVDSGVEPIDGIVLDEYIRNRKVFQIV 58
DB 189 KVIQCYQDNHNLGNGSAPSPFLCAMQLFSHMHAV--ISTYCKRHSFIQSTFSINPEIV 246
QY 59 CSFRGDEDEVMGLNFQKELCLASSEQIYPRPE-KSDKEQTKLOERLLKLGSNAPPTF 117
DB 247 C-----DPLSDYNWMSMKPINTSYGLEPDVRRVVAARLRSR-----SPFW 288
QY 118 NISNAPBSVTLOQGEDNDGPCGVSYVKIPAGESETDRHRSSTVTLGIRKIOFA--- 174
DB 289 NVADGAESA-ASFTVQLAAEA---LHKA PDVTTLSRNVWFVFFQ 330
QY 175 -----PTKGOOPCTLVKRDPMFLSGELEVTLDKOLYHGERIGVNICI 220
DB 331 GETFDYIGSSHMVYDMENKFPVRLENIDSFVEJQVLRSLD-LMMH----- 378
QY 221 RNSNKKVKKIKAMVOQVDVLFQNGSYRNTVASLET-SGCP-----IOPGS 268
DB 379 ---IDPMQKVESYKQVEDL-----LATLEKSGAGVEVRLAQSALPPS 424
QY 269 SLQKVM 274
DB 425 SLQKFL 430

RESULT 10
US-10-505-928-304
; Sequence 304, Application US/10505928
; Publication No. US20060086532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 304
; LENGTH: 763
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-304

Query Match 3.7%; Score 73; DB 6; Length 763;
Best Local Similarity 19.4%; Pred. No. 7.4;
Matches 63; Conservative 46; Mismatches 120; Indels 96; Gaps 15;

QY 83 SEQIYPRPKSDKEQTKLOERLLKLG-SNAIPFTFNT-----SNA 123
DB 25 SETSEBPKRSPAQOESQAESKESVANSCKFPAGIKIINHPTMPTQVVAIPNNANT 84
QY 124 PSSVTLOQGEDNDGPCGVSYVKIFAG-----ESRTDRHRSSTVTLGIRKIQ 172
DB 85 HSIIITLAKKESSESSGPKRILISCGAPPTOPGRLQRTOTSYDAKTEVTL----- 138
QY 173 FAPTKGOOPCTLVKRDPMFL--SPG--ELELEVTLDKOLYHGERIGVNICIRNNSNM 227
DB 139 ---ETLGPAPAA---RDVNLPRPPALCEQKRETCAD-----GEAAG---CTINNSLN 183
QY 228 VKKIAMVOQVDVLFQNGSYRNTVASLETSEGCPIQSGSSLOKMYITPLSSNKKOR 287
DB 184 IQMLKRMSSDGL-----GS-RSIKQENKEKENCLE-----QR- 215
QY 288 GIALGOIKRDOCLASTTLAQPDORDAFG--VIISYAV---KVKFLGALGELSAE 341
DB 216 -----QVVEBPSRPSASWQNSVSRPPYSYMIQFALINSTRERKMTLKDIYTWIEDH 269

QY 342 LPFVLMHPRKPTKAKVTHADSOADV 366
DB 270 PFYFKHIAKPKGKXNSIRHNLSDHW 294

RESULT 11
US-11-251-465-22
; Sequence 22, Application US/11251465
; Publication No. US20060094061A1
; GENERAL INFORMATION:
; APPLICANT: Brys, Reginald
; APPLICANT: Vandeghinste, Nick
; APPLICANT: Tonne, Peter
; APPLICANT: Klaassen, Hubertus
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
; TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
; FILE REFERENCE: P30,172-A USA
; CURRENT APPLICATION NUMBER: US/11/251,465
; CURRENT FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: 60/619,384
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 880
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 806
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-251-465-22

Query Match 3.7%; Score 72.5; DB 7; Length 806;
Best Local Similarity 18.3%; Pred. No. 9.2;
Matches 81; Conservative 73; Mismatches 145; Indels 143; Gaps 22;

QY 11 CAPNGKTYLVGKDFVDHVSVEPIDGIYV-----LDDEYIRNRKVFQIV 58
DB 61 CPPPGGCP--MGPIVWVKDGLVPSRVIAVGPQRLVLANSHBDSGASCRORLTVL 118
QY 59 CSFRY-----GREDEVMGLNFQKELCLASSEQIYPRPKSDKEQTKLOERLL 105
DB 119 CHFSVRVTDAPSSGDEDEDEDEADTGVD-----TGAPYWTPEPRMDK-----KTL 164
QY 106 KKLGSNAIPFTFNTSPN-APSSVTLOQGEDNDGPCGVSYVKIPAGESETDRHRSST 164
DB 165 AVPAANTVFRCPAAGNTPSISWLKGRB-----FRGE-----HRIGGI 204
QY 165 TLGIRKIOFA-----PTKGOOPCTV-----VRKDFML-----SPGELEVTLD-K 205
DB 205 KL--RHQWMSLWMSVPSDRGNTCVENKFGSIRQTYTLDVLESPHPILOGLPAN 262
QY 206 QLYHGERIGVNICIRNNSNMVKKIKAMVOQVDVLFQNGSYRNTVASLETSGCTIQ 265
DB 263 QTAVALGSDVEFHCKVYSDAOPHIOMLKXIVNYSKV-----GPDGTP-- 304
QY 266 PGSSLOKMYITPL-----SSNKORGIALDGOIKROD-----OCLASTTL----- 307
DB 305 -----YVTLKTAGANTTDKELEVLISLH-NVTEFDABEYICLAQNSIGFSHSGAWL 354
QY 308 -----LAOPDR-DAFGVIISYAVKVLFLGALGELSABE.PFVLMHPRKPTKARVI 358
DB 355 VVLPABEELVEADEGSAVYAGILSYGVGFILVVA---AVTLCLRLSPKKGIGSPTV 411
QY 359 HADSOADVETTRQDTIIDQASV 380
DB 412 HKISRFPK--ROVSLBSNASM 431

RESULT 12
US-10-322-836-48
; Sequence 48, Application US/10322836
; Publication No. US20060090212A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Alexander C., Jr.

APPLICANT: Zambrowicz, Brian
APPLICANT: Nehls, Michael
APPLICANT: Freidrich, Glenn A.
APPLICANT: Sande, Arthur T.
TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
FILE REFERENCE: 8535-0037-999
CURRENT APPLICATION NUMBER: US/10/322,836
PRIOR FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: US/09/579,114
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 48
LENGTH: 1075
TYPE: PRT
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: SITE
LOCATION: (130)...(130)
OTHER INFORMATION: Xaa = Gln or STOP
FEATURE:
NAME/KEY: SITE
LOCATION: (179)...(179)
OTHER INFORMATION: Xaa = Ser or Gly
US-10-322-836-48

Query Match 3.7%; Score 72.5; DB 6; Length 1075;
Best Local Similarity 16.8%; Pred. No. 15;
Matches 48; Conservative 48; Mismatches 94; Indels 95; Gaps 11;

17 VTLVGMGRDPVDFHVSQVPEIDGIVLDEYIRD---NRKFGQIVCSFRYGRDEDEVMG 72
101 LVHQTRESRDAT-----LNDIFMNNVYALSKISEVILIFPKSKNE-----IG 146
QY 73 LNFQKELCLASEQIYP-----RPKSDKEQTKLQERLKKLGSMALPFTFNT 119
147 LQNHBEELKTYNLELYTKTYHMYHASEISAEKXKLKAEKQEFKNGSD----- 197
QY 120 SPNAPSVTLOQGGDDMGDCGVSYYKIFAGESETRTRHRSVTLGIRKIQAPRK-- 177
198 ----LSMNLIRHE-----DRPQRSSV---KKLEKMKERQ 226
QY 178 ----QGQPCPTLVKDFMLSPGELEBVTLDKQYLHGERIGVNICIRNNSNMVKKIXA 233
227 AKYSENKLTCKTKRANVDYLLMLAATNAIS---KYIHVDGDLIDCCGLGFHASLARTFRT 283
QY 234 MV-----QGQVDVY-----LFQNGSYRNTVASLETSEGCP 263
284 YLSAEVNLLETSRHGLDVIENAVDNLDSRDKHTVMDCMQVFCP 328
DB

RESULT 13
US-10-505-928-310
Sequence 310, Application US/10505928
Publication No. US20060088532A1
GENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research et al.
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39178
CURRENT APPLICATION NUMBER: US/10/505,928
PRIOR FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: PatentIn 3.2
SEQ ID NO 310
LENGTH: 2215
TYPE: PRT
ORGANISM: Homo sapiens
US-10-505-928-310

Query Match 3.7%; Score 72.5; DB 6; Length 2215;

Best Local Similarity 21.4%; Pred. No. 52;
Matches 86; Conservative 50; Mismatches 137; Indels 129; Gaps 22;
QY 12 APNGKTYLVMGKDPFDHVSQVPEIDGIVLDEYIRD--NRKFGQIVCSFRYGR----- 65
DB 963 APGFEDLERGRREWE-----EDLDAALPLPEDEEDISEYKFAKFAATYFGGTTTSHY 1017
QY 66 -----BEDE-----VMGLNFQKELCLASEQIYPRPE-----KSDKEQ--- 97
DB 1018 TRRPLKQPLLYHDEBDQALAAVWITILRFMDL-----PEKKYHTANSDSGSEKIP 1069
QY 98 --TKLQERLIKKGSNALPFTFENISPNAPSVTLOQGGDDNGDPCG-----VS 143
DB 1070 VMTKIYETLGKK-----TYK-----RELQALQGEQAQIPESQKKSVMHKLVLHT 1115
QY 144 YVYKIFAGESETRTRHRSVTLGIRKIQAPRKQGOQPCITVRKDFMLSPGEL----- 197
DB 1116 LKKSKLTBEVTRKRLHDSESTVOGNSMLEDRPTS-----NLEKLFITGILRALRD 1169
QY 198 ELEVTLDKQI-----YLHGERIGVNICIR--NNSNMVKKIKAMVOQG--VDVVLFOV 246
DB 1170 EIVCOISKQLTNHPKSSVARG--WILVSLCVGCFAPSEKRVKYLRFHIGGPPGYAPYCE 1228
QY 247 GSYRNTVASLETSEGCPIDQSSLGQKVMYLTPLSSNKQRRGIAL-----DQIKRQDOC 301
DB 1229 ERLRRITFVN-----GTRQPPSWLE-----LQATKSKKPIMLVTFMDGTTKTLTD 1275
QY 302 LAST-----TLAQRDQRPAGFVIVSYAVKVLF--LGALG 335
DB 1276 SATTAKELCNALDKISLKDPRF---FSLYIALPKVSVSLG 1313

RESULT 14
US-10-511-937-2451
Sequence 2451, Application US/10511937
Publication No. US2006008836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgenuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, Macdonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
PRIOR FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR APPLICATION NUMBER: US 10/325,899
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2451
LENGTH: 798
TYPE: PRT
ORGANISM: Homo sapiens
US-10-511-937-2451

Query Match 3.6%; Score 71; DB 6; Length 798;
Best Local Similarity 19.7%; Pred. No. 13;
Matches 43; Conservative 33; Mismatches 88; Indels 54; Gaps 8;

QY 48 RDRNKYVGOIIVCSFRYGRDEDEVMGILNFQKELCLASEQIYPRPKSDKEQTKLQERLKL- 106
DB 8 QDSSEVWSDEICAAVLGDED-----PLC-----PDLBELDLSLVDVNDLDT 48
QY 107 -----KLGSNALPFTFENISPNAPSVTLOQGGDDNG-----DPCGVSY 144

Db 49 DSFLGKMCSDQGEIISNQYNNEPSNIFEKIDENENALLAVLTETIDSLPVEDGLPS 108
QY 145 YKIFAGESETDRTHRRSTVTTLGIRKIQFAPTKOQOQPCTLVRKDFMLSPGELELEVY-- 202
Db 109 FDALTDGVTVDNENASPSMFDGT-----PPQENRPSLL--KKLLAPANTQLSYNEC 161
QY 203 --LDKQLYL-HGERIGVNICIRNNSNKKVKKIKAMVQ 237
Db 162 SGLSTQNHANHNHRIRTNPAIVKTEMSWSNKAKSICQ 199

RESULT 15

US-11-316-132-1
; Sequence 1, Application US/11316132
; Publication No. US20060100153A1
; GENERAL INFORMATION:
; APPLICANT: Shridhar, Vijj
; APPLICANT: Roberts, Lewis R.
; APPLICANT: Kaufmann, Scott H.
; TITLE OF INVENTION: HSulf-1 Nucleic Acids, Polypeptides and
; FILE REFERENCE: 07039/449001
; CURRENT APPLICATION NUMBER: US/11/316,132
; PRIOR FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/778,607
; PRIOR FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 60/446,945
; PRIOR FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-316-132-1

Query Match 3.6%; Score 71; DB 7; Length 871;
Best local Similarity 28.6%; Pred. No. 15;
Matches 30; Conservative 16; Mismatches 35; Indels 24; Gaps 6;

QY 6 KVFKKC--APNGKV-----TLYMGKRDFTVDHVSQVEPIDGIIVLDEYIRDNRYGGOIVC 59
Db 613 RVTHKCFILPNDSTICERELYQSAWAKDHAKYID--KEIALQDK-IKNLREVRGHL-- 667
QY 60 SFRYGRBEDEVYGLNFQKELCLASEQIYPRPEKSDPEQTKLQERL 104
Db 668 ---KRRKPE-----CSCSKQSYNNKEKGVKKQEKLSHL 699

Search completed: May 20, 2006, 23:06:54
Job time : 12 secs

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OM protein - protein search, using 6w model

Run on: May 20, 2006, 23:06:58 ; Search time 196 Seconds
(without alignments)
893.438 Million cell updates/sec

Title: US-10-056-405-2

Perfect score: 383
Sequence: 1 MVMFKVKKCAPNGKTLT.....ADVETPRODTIDQASVDFE 383

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 2589679 seqs, 457216429 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2589203

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

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1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	383	100.0	383	5	ABP52833
2	383	100.0	383	7	ABR84476
3	20	5.2	364	4	ABR61736
4	20	5.2	364	4	ADO89588
5	11	2.9	382	4	AA667785
6	11	2.9	398	7	ABR84484
7	11	2.9	401	4	ABR61964
8	11	2.9	409	4	AA667784
9	11	2.9	409	7	AA667781
10	11	2.9	409	7	AD58183
11	11	2.9	409	7	AD58179
12	11	2.9	409	7	ADN95251
13	11	2.9	409	5	ADY15068
14	11	2.9	410	5	ABG69496
15	11	2.9	410	7	AD58177
16	11	2.9	410	7	AD58181
17	11	2.9	479	10	ABR35190
18	11	2.9	492	10	ABR35191
19	11	2.9	526	8	ADR23187
20	11	2.9	526	8	ADR23188
21	11	2.9	526	8	ADR23186
22	9	2.3	388	4	AA667782
23	9	2.3	388	4	AA667783

24	9	2.3	388	9	ADX07504
25	9	2.3	394	9	AED51702
26	9	2.3	470	4	ABR58174
27	8	2.1	22	7	ADU94231
28	8	2.1	38	4	AAAM20580
29	8	2.1	38	4	ABR41697
30	8	2.1	38	4	AAAM35493
31	8	2.1	38	4	ABR25470
32	8	2.1	38	4	AAAM75381
33	8	2.1	38	4	AAAM62570
34	8	2.1	38	4	ABG57138
35	8	2.1	38	5	ABG44975
36	8	2.1	180	6	ADA00634
37	8	2.1	182	7	ADD27419
38	8	2.1	182	7	ADD27127
39	8	2.1	182	7	ADD27197
40	8	2.1	187	6	ABU70623
41	8	2.1	187	7	ADD27507
42	8	2.1	204	2	AAW20559
43	8	2.1	204	2	AAW24688
44	8	2.1	212	4	AA673899
45	8	2.1	279	7	ABO78668

ALIGNMENTS

RESULT 1
ABP52833
ID ABP52833 standard; protein; 383 AA.
XX
AC ABP52833;
XX
DT 01-NOV-2002 (first entry)
XX
DE Anopheles gambiae arreslin 1 protein SEQ ID NO:2.
XX
DE Anopheles gambiae; mosquito; olfactory gene; arreslin 1; pest control;
XX
KW odorant receptor; olfaction.
XX
OS Anopheles gambiae.
XX
PN WO200259274-A2.
XX
PD 01-AUG-2002.
XX
PF 28-JAN-2002; 2002WO-US002549.
XX
PR 26-JAN-2001; 2001US-026649P.
XX
PR 24-JAN-2002; 2002US-00056405.
XX
(UYVA-) UNTV VANDERBILT.
XX
PI Zwiebel LJ;
XX
DR WPI: 2002-627421/67.
XX
DR N-PSDB: ABQ75102.
XX
PT New mosquito olfaction polypeptides and polynucleotides, useful for
PT mosquito management, i.e. controlling the pest and disease vectors, or
PT for identifying pest control agents.
XX
PS Claim 18; Fig 2; 96pp; English.
XX
CC The present invention describes a purified Anopheles gambiae olfaction
CC polypeptide comprising a 383, 394, 380, 411, 412, 391, 157 or 401 residue
CC amino acid sequence (see ABP52833 to ABP52840) (S1), a conservatively
CC modified amino acid sequence of them, or a sequence of (S1) with at least
CC 20 consecutive residues. Also described: (i) an isolated polynucleotide
CC comprising: (a) a nucleotide sequence encoding the purified Anopheles
CC gambiae olfaction polypeptide; or (b) a nucleotide sequence that
CC hybridizes under stringent conditions to a hybridisation probe comprising
CC a 1964, 1239, 1142, 1236, 1194, 1176, 474 or 1206 nucleotide sequence

(see AB075102 to AB075105 and AB075110 to AB075113) (S2), or its complement; and (2) a method for identifying an agent that binds to mosquito olfaction molecules comprising: (a) providing an isolated mosquito olfaction molecule; (b) contacting a test agent with the isolated mosquito olfaction molecule; and (c) detecting specific binding of the test agent to the isolated mosquito olfaction molecule, where the presence of specific binding identifies the test agent as a mosquito olfaction-binding compound. The mosquito olfaction molecules are useful for mosquito management, i.e. controlling this pest and disease vector. A method from the present invention of screening for substances that modulate arrestin-odorant receptor interaction is useful for identifying pest control agents. The present sequence represents Anopheles gambiae arrestin 1 from the present invention

Sequence 383 AA;

Query Match 100.0%; Score 383; DB 5; Length 383;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVYVFKVFKKCAPNGKVTLYMGKRFVDHVSVEPIDGIVLDDYIRDNKRVGQIVCS 60
DB 1 MVYVFKVFKKCAPNGKVTLYMGKRFVDHVSVEPIDGIVLDDYIRDNKRVGQIVCS 60
QY 61 FRYGREDEWVGLNFOKELCLASEQIYPRPEKSKDEQTKLOERLLKLGSAIPTFNIS 120
DB 61 FRYGREDEWVGLNFOKELCLASEQIYPRPEKSKDEQTKLOERLLKLGSAIPTFNIS 120
QY 121 PNAISSVTLLQOGEDNDGPGCVSYVVKIPAGESETDRTHRSVTYLGIRKIQFAPTKQGQ 180
DB 121 PNAISSVTLLQOGEDNDGPGCVSYVVKIPAGESETDRTHRSVTYLGIRKIQFAPTKQGQ 180
QY 181 QPCTLVKRD FMLSPELELEVTLDKQYLHGERIGVNICIRNNSKNKWKIKAMVQGVND 240
DB 181 QPCTLVKRD FMLSPELELEVTLDKQYLHGERIGVNICIRNNSKNKWKIKAMVQGVND 240
QY 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOKWMYLTPLSSNKQRGIALDGOIKRQDQ 300
DB 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOKWMYLTPLSSNKQRGIALDGOIKRQDQ 300
QY 301 CLASTTLLAOPDQDAFGVIISYAVKVLFLGALGELSABLPLVLMHPKPGTAKVIHA 360
DB 301 CLASTTLLAOPDQDAFGVIISYAVKVLFLGALGELSABLPLVLMHPKPGTAKVIHA 360
QY 361 DSQADVETFRQDTIDQASVDPE 383
DB 361 DSQADVETFRQDTIDQASVDPE 383

RESULT 2

ABR84476 ID ABR84476 standard; protein; 383 AA.

AC ABR84476;

DT 15-JAN-2004 (first entry)

DE Mosquito olfaction molecule, arrestin 1.

KW Arrestin 1; mosquito; olfaction; insecticide; antimalarial.

OS Anopheles gambiae.

PN WO2003076590-A2.

PD 18-SEP-2003.

PF 10-MAR-2003; 2003WO-US007174.

PR 08-MAR-2002; 2002US-00094240.

XX (UYVA-) UNIV VANDERBILT.

XX PA

PI Zwiebel LJ;

XX MPI; 2003-722331/68.

DR N-PSDB; ACF79716.

XX New mosquito arrestin 1 and 2 genes and polypeptides, useful for

PT identifying mosquito olfaction molecule binding compounds which reduce

XX the ability of mosquitoes to locate sources of bloodmeal, e.g. humans.

PS Claim 1; Fig 2; 101bp; English.

CC The present sequence is the protein sequence of arrestin 1, a novel
CC mosquito olfaction molecule. The invention provides 9 novel mosquito
CC polypeptides and the nucleic acids encoding them. These are arrestins 1
CC and 2 and odorant receptor molecules 1-7. The odorant receptors function
CC in a ligand-induced signal transduction pathway for the activation of
CC mosquito olfaction. Arrestin functions to inhibit the activated signal
CC transduction cascade. Thus, the odorant receptors act as an 'on' switch,
CC and arrestin as an 'off' switch for the odorant detection system of the
CC mosquito. Methods are provided for identifying compounds that interfere
CC with the operation of the mosquito olfactory system, particularly
CC compounds that modulate arrestin 2 activity. These are useful for the
CC control of mosquitoes, particularly by reducing their ability to locate
CC sources of bloodmeal

Sequence 383 AA;

Query Match 100.0%; Score 383; DB 7; Length 383;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVYVFKVFKKCAPNGKVTLYMGKRFVDHVSVEPIDGIVLDDYIRDNKRVGQIVCS 60
DB 1 MVYVFKVFKKCAPNGKVTLYMGKRFVDHVSVEPIDGIVLDDYIRDNKRVGQIVCS 60
QY 61 FRYGREDEWVGLNFOKELCLASEQIYPRPEKSKDEQTKLOERLLKLGSAIPTFNIS 120
DB 61 FRYGREDEWVGLNFOKELCLASEQIYPRPEKSKDEQTKLOERLLKLGSAIPTFNIS 120
QY 121 PNAISSVTLLQOGEDNDGPGCVSYVVKIPAGESETDRTHRSVTYLGIRKIQFAPTKQGQ 180
DB 121 PNAISSVTLLQOGEDNDGPGCVSYVVKIPAGESETDRTHRSVTYLGIRKIQFAPTKQGQ 180
QY 181 QPCTLVKRD FMLSPELELEVTLDKQYLHGERIGVNICIRNNSKNKWKIKAMVQGVND 240
DB 181 QPCTLVKRD FMLSPELELEVTLDKQYLHGERIGVNICIRNNSKNKWKIKAMVQGVND 240
QY 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOKWMYLTPLSSNKQRGIALDGOIKRQDQ 300
DB 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOKWMYLTPLSSNKQRGIALDGOIKRQDQ 300
QY 301 CLASTTLLAOPDQDAFGVIISYAVKVLFLGALGELSABLPLVLMHPKPGTAKVIHA 360
DB 301 CLASTTLLAOPDQDAFGVIISYAVKVLFLGALGELSABLPLVLMHPKPGTAKVIHA 360
QY 361 DSQADVETFRQDTIDQASVDPE 383
DB 361 DSQADVETFRQDTIDQASVDPE 383

RESULT 3

ABB61736 ID ABB61736 standard; protein; 364 AA.

AC ABB61736;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 12000.

KW Drosophila; developmental biology; cell signalling; insecticide;

XX KM

XX PA

OS Drosophila melanogaster.
 XX WO200171042-A2.
 XX 27-SEP-2001.
 XX 23-MAR-2001; 2001WO-US009221.
 XX 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX (PEKE) PE CORP NY.
 XX Venter JC, Adams M, Li PWD, Myers EW;
 PI WPI; 2001-656680/75.
 DR N-PSDB; ABL05839.
 DR
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 PS Disclosure; SEQ ID NO 12000; 21pp + Sequence listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signaling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
 CC ABB12072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 364 AA;

Query Match 5.2%; Score 20; DB 4; Length 364;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 228 VKKIKAMVQGVVVLFPONG 247
 |||||
 DB 227 VKKIKAMVQGVVVLFPONG 246

RESULT 4
 ADQ89588
 ID ADQ89588 standard; protein; 364 AA.
 XX
 AC ADQ89588;
 XX
 AC
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Antagonist of cell cycle progression polypeptide #9.
 XX
 KW Cytostatic; cancer; cell division cycle; mitosis; meiosis;
 KW cell cycle progression.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO2004063362-A2.
 XX
 PD 29-JUL-2004.
 XX
 PF 31-DEC-2003; 2003WO-GB005635.
 XX
 PR 10-JAN-2003; 2003US-0439123P.
 PR 06-MAY-2003; 2003US-0468402P.
 XX
 PA (CYCL-) CYCLACEL LTD.
 XX
 PI Glover D, Bell G, Frenz L, Midgley C;

XX WPI; 2004-544089/52.
 DR N-PSDB; ADQ89587.
 DR
 XX New cell cycle progression genes and proteins for modulating cell cycle
 PT progression in cells, for preventing, treating or diagnosing cell
 PT proliferative diseases (e.g. cancer) or for identifying modulators of
 PT mitosis or meiosis.
 XX
 PS Claim 2; SEQ ID NO 18; 461pp; English.
 XX
 CC The present invention relates to a polynucleotide for preventing,
 CC treating or diagnosing a disease in an individual. The composition or the
 CC polypeptide, polynucleotide or RNA precursor, or antibody is useful for
 CC diagnosing, preventing or treating diseases (e.g. cell proliferative
 CC diseases such as cancer) in an individual. These may also be used for
 CC identifying substances capable of binding to or modulating the function
 CC of the polypeptide, capable of affecting the function of the
 CC corresponding gene, or capable of inhibiting the cell division cycle or
 CC cell cycle progression, preferably mitosis and/or meiosis. The present
 CC sequence represents an antagonist of cell cycle progression protein
 CC sequence.
 CC
 SQ Sequence 364 AA;

Query Match 5.2%; Score 20; DB 8; Length 364;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 228 VKKIKAMVQGVVVLFPONG 247
 |||||
 DB 227 VKKIKAMVQGVVVLFPONG 246

RESULT 5
 AAG67785
 ID AAG67785 standard; protein; 382 AA.
 XX
 AC AAG67785;
 XX
 DT 10-DEC-2001 (first entry)
 XX
 DE An exemplary phosphorylation-independent arrestin mutant.
 XX
 DE Arrestin; phosphorylation-independent arrestin mutant;
 KW G protein-coupled receptor; GPCR; GPCR ligand; retinitis pigmentosa;
 KW stationary night blindness; colour blindness; nephrogenic DI;
 KW isolated glucocorticoid deficiency; hyperfunctioning thyroid adenoma;
 KW familial hypocalcaemic hypocalcaemia; hyperparathyroidism;
 KW neurological disorder.
 XX
 OS Unidentified.
 XX
 PN WO200167106-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 05-MAR-2001; 2001WO-US007304.
 XX
 PR 03-MAR-2000; 2000US-0186706P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Berstein G;
 XX
 DR WPI; 2001-602637/68.
 XX
 PT Identifying a G protein-coupled receptor ligand, useful for treating e.g.
 PT retinitis pigmentosa, color blindness or neurological disorders, uses
 PT phosphorylation-independent arrestin mutants particularly suited for in
 PT vitro screening assays.
 XX
 PS Disclosure; Page 47; 47pp; English.

XX The present sequence represents an exemplary phosphorylation-independent
 CC arrestin mutant. Such mutants are used in screening assays to identify
 CC ligands and/or modulators of G protein-coupled receptors (GPCRs). A
 CC method for identifying a GPCR ligand comprises contacting a composition
 CC comprising the GPCR and a constitutively active arrestin mutant with a
 CC test compound; and determining the ability of the test compound to
 CC modulate binding of arrestin mutant to the GPCR, where modulation of
 CC binding indicates that the test compound is a GPCR ligand. The method is
 CC used for identifying potential ligands and/or modulators of GPCRs,
 CC particularly modulators, for use as human therapeutics. Modulators of
 CC GPCR may be used for treating patients having e.g. retinitis pigmentosa,
 CC stationary night blindness, colour blindness, nephrogenic DI, isolated
 CC glucocorticoid deficiency, hyperparathyroidism and neurological
 CC hypocalcaemic hypercalcaemia, hyperparathyroidism and neurological
 CC disorders. The methods may be used for screening pluralities of test
 CC compounds (e.g. a small molecule library of compounds) or a composition
 CC containing a plurality of GPCRs. The methods may be used in screening
 CC assays for identification of natural and surrogate agonists of orphan
 CC GPCRs, and for identification of GPCR antagonists and/or agonists

XX Sequence 382 AA;

Query Match 2.9%; Score 11; DB 4; Length 382;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 ELFPVLMHPKP 351
 |||||
 DB 339 ELFPVLMHPKP 349

RESULT 6

ABR84484 ABR84484 standard; protein; 398 AA.

XX ABR84484;

XX 15-JAN-2004 (first entry)

XX Mosquito olfaction molecule; arrestin 2.

XX Arrestin 2; mosquito; olfaction; insecticide; antimalarial.

XX Anopheles gambiae.

XX Key Location/Qualifiers

XX FT Misc-difference 152 /note= "Encoded by AG"

XX WO2003076590-A2.

XX 18-SEP-2003.

XX 10-MAR-2003; 2003WO-US007174.

XX 08-MAR-2002; 2002US-00094240.

XX (UYVA-) UNIV VANDERBILT.

XX Zwiebel LJ;

XX MPI; 2003-722331/68.

XX N-PSDB; AC79731.

XX New mosquito arrestin 1 and 2 genes and polypeptides, useful for
 PT identifying mosquito olfaction molecule binding compounds which reduce
 PT the ability of mosquitoes to locate sources of bloodmeal, e.g. humans.

XX Claim 16; Fig 12b; 101pp; English.

XX The present sequence is the protein sequence of arrestin 2, a novel
 CC mosquito olfaction molecule. The invention provides 9 novel mosquito

CC polypeptides and the nucleic acids encoding them. These are arrestins 1
 CC and 2 and odorant receptor molecules 1-7. The odorant receptors function
 CC in a ligand-induced signal transduction pathway for the activation of
 CC mosquito olfaction. Arrestin functions to inhibit the activated signal
 CC transduction cascade. Thus, the odorant receptors act as an 'on' switch,
 CC and arrestin as an 'off' switch for the odorant detection system of the
 CC mosquito. Methods are provided for identifying compounds that interfere
 CC with the operation of the mosquito olfactory system, particularly
 CC compounds that modulate arrestin 2 activity. These are useful for the
 CC control of mosquitoes, particularly by reducing their ability to locate
 CC sources of bloodmeal

XX Sequence 398 AA;

Query Match 2.9%; Score 11; DB 7; Length 398;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 RYGREDEWVG 72
 |||||
 DB 61 RYGREDEWVG 71

RESULT 7

ABB61964 ABB61964 standard; protein; 401 AA.

XX ABB61964;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 12684.

XX Drosophila: developmental biology; cell signalling; insecticide;

XX pharmaceutical.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

XX 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX MPI; 2001-656860/75.

XX N-PSDB; ABL06067.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.

XX Disclosure; SEQ ID NO 12684; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01940-ABL16175) and the encoded proteins (ABBS7737-
 CC AB872072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 401 AA;

Query Match 2.9%; Score 11; DB 4; Length 401;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 62 RYGREDEVMG 72
 Db 61 RYGREDEVMG 71

RESULT 8

AA67784
 ID AA67784 standard; protein; 409 AA.

AC AAG67784;
 XX

DT 10-DEC-2001 (first entry)
 XX

DE An exemplary phosphorylation-independent arrestin mutant.

XX Arrestin; phosphorylation-independent arrestin mutant;

KW G protein-coupled receptor; GPCR; GPCR ligand; retinitis pigmentosa;
 KW stationary night blindness; colour blindness; nephrogenic DI;
 KW isolated glucocorticoid deficiency; hyperfunctioning thyroid adenoma;
 KW familial hypocalcaemic hypercalcaemia; hyperparathyroidism;
 KW neurological disorder.

KM
 KM
 XX

OS Unidentified.
 XX

PN MO200167106-A2.
 XX

PD 13-SEP-2001.
 XX

PF 05-MAR-2001; 2001WO-US007304.
 XX

PR 03-MAR-2000; 2000US-0186706P.
 XX

PA (MILL-) MILLENNIUM PHARM INC.
 XX

PI Berestein G;
 XX

DR WPI; 2001-602637/68.
 XX

PT Identifying a G protein-coupled receptor ligand, useful for treating e.g.
 PT retinitis pigmentosa, color blindness or neurological disorders, uses
 PT phosphorylation-independent arrestin mutants particularly suited for in
 PT vitro screening assays.

PS Disclosure; Page 47; 47pp; English.
 XX

XX The present sequence represents an exemplary phosphorylation-independent
 XX arrestin mutant. Such mutants are used in screening assays to identify
 XX ligands and/or modulators of G protein-coupled receptors (GPCRs). A
 XX method for identifying a GPCR ligand comprises contacting a composition
 XX comprising the GPCR and a constitutively active arrestin mutant with a
 XX test compound; and determining the ability of the test compound to
 XX modulate binding of arrestin mutant to the GPCR, where modulation of
 XX binding indicates that the test compound is a GPCR ligand. The method is
 XX used for identifying potential ligands and/or modulators of GPCRs,
 XX particularly modulators, for use as human therapeutics. Modulators of
 XX GPCR may be used for treating patients having e.g. retinitis pigmentosa,
 XX stationary night blindness, colour blindness, nephrogenic DI, isolated
 XX glucocorticoid deficiency, hyperfunctioning thyroid adenomas, familial
 XX hypocalcaemic hypercalcaemia, hyperparathyroidism and neurological
 XX disorders. The methods may be used for screening pluralities of test
 XX compounds (e.g. a small molecule library of compounds) or a composition
 XX containing a plurality of GPCRs. The methods may be used in screening
 XX assays for identification of natural and surrogate agonists of orphan
 XX GPCRs, and for identification of GPCR antagonists and/or agonists

XX Sequence 409 AA;
 SQ

Query Match 2.9%; Score 11; DB 4; Length 409;
 Best Local Similarity 100.0%; Pred. No. 0.13;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 341 ELFPVLMHPR 351
 Db 339 ELFPVLMHPR 349

RESULT 9

AA67781
 ID AA67781 standard; protein; 409 AA.

AC AAG67781;
 XX

DT 10-DEC-2001 (first entry)
 XX

DE Amino acid sequence of human beta-arrestin 2.

XX Arrestin; phosphorylation-independent arrestin mutant;

KW G protein-coupled receptor; GPCR; GPCR ligand; retinitis pigmentosa;
 KW stationary night blindness; colour blindness; nephrogenic DI;
 KW isolated glucocorticoid deficiency; hyperfunctioning thyroid adenoma;
 KW familial hypocalcaemic hypercalcaemia; hyperparathyroidism;
 KW neurological disorder.

KM
 KM
 XX

OS Homo sapiens.
 XX

FN Key Location/Qualifiers
 FT Region 156..185
 FT /note="putative phosphorylation-recognition region"

PN MO200167106-A2.
 XX

PD 13-SEP-2001.
 XX

PF 05-MAR-2001; 2001WO-US007304.
 XX

PR 03-MAR-2000; 2000US-0186706P.
 XX

PA (MILL-) MILLENNIUM PHARM INC.
 XX

PI Berestein G;
 XX

DR WPI; 2001-602637/68.
 XX

PT Identifying a G protein-coupled receptor ligand, useful for treating e.g.
 PT retinitis pigmentosa, color blindness or neurological disorders, uses
 PT phosphorylation-independent arrestin mutants particularly suited for in
 PT vitro screening assays.

PS Disclosure; Page 46; 47pp; English.
 XX

XX The present sequence represents an arrestin protein. The specification
 XX describes phosphorylation-independent arrestin mutants. These mutants are
 XX used in screening assays to identify ligands and/or modulators of G
 XX protein-coupled receptors (GPCRs). A method for identifying a GPCR ligand
 XX comprises contacting a composition comprising the GPCR and a
 XX constitutively active arrestin mutant with a test compound; and
 XX determining the ability of the test compound to modulate binding of
 XX arrestin mutant to the GPCR, where modulation of binding indicates that
 XX the test compound is a GPCR ligand. The method is used for identifying
 XX potential ligands and/or modulators of GPCRs, particularly modulators,
 XX for use as human therapeutics. Modulators of GPCR may be used for
 XX treating patients having e.g. retinitis pigmentosa, stationary night
 XX blindness, colour blindness, nephrogenic DI, isolated glucocorticoid
 XX deficiency, hyperfunctioning thyroid adenomas, familial hypocalcaemic
 XX hypercalcaemia, hyperparathyroidism and neurological disorders. The
 XX methods may be used for screening pluralities of test compounds (e.g. a
 XX small molecule library of compounds) or a composition containing a
 XX plurality of GPCRs. The methods may be used in screening assays for
 XX identification of natural and surrogate agonists of orphan GPCRs, and for
 XX identification of GPCR antagonists and/or agonists

XX Sequence 409 AA;
 SQ

Query Match 2.9%; Score 11; DB 4; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 ELFPVLMHMKP 351
|||
339 ELFPVLMHMKP 349

RESULT 10
ADES8183
ID ADE58183 standard; protein; 409 AA.

XX ADE58183;

DT 29-JAN-2004 (first entry)

DE Human Protein P32121, SEQ ID NO 4054.

XX Human; pain; neuronal tissue; gene therapy;

KM spinal segmental nerve injury; chronic constriction injury; CCI;

XX spared nerve injury; SNI; Chung.

OS Homo sapiens.

XX WO2003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

PI Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

DR GENBANK; P32121.

XX New composition comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat

CC or human polynucleotides or a polynucleotide which represents a fragment,

CC derivative or allelic variation of the nucleic acid sequence. Also

CC claimed are a vector comprising the novel polynucleotide, a host cell

CC comprising the vector, a method for identifying a nucleotide sequence

CC which is differentially regulated in an animal subjected to pain and a

CC kit to perform the method, an array, a method for identifying an agent

CC that increases or decreases the expression of the polynucleotide sequence

CC that is differentially expressed in neuronal tissue of a first animal

CC subjected to pain, a method for identifying a compound which regulates

CC the expression of a polynucleotide sequence which is differentially

CC expressed in an animal subjected to pain, a method for identifying a

CC compound that regulates the activity of one or more of the

CC polynucleotides, a method for producing a pharmaceutical composition, a

CC method for identifying a compound or small molecule that regulates the

CC activity in an animal of one or more of the polypeptides given in the

CC specification, a method for identifying a compound useful in treating

CC pain and a pharmaceutical composition comprising the one or more

CC polypeptides or their antibodies. The polynucleotide or the compound that

CC modulates its activity is useful for preparing a medicament for treating

CC pain (e.g. spinal segmental nerve injury (SNI), chronic constriction

CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene

CC therapy). The sequence presented is a human protein (shown in table 2 of

CC the specification) which is differentially expressed during pain. Note:

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic form directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 409 AA;

QY 341 ELFPVLMHMKP 351
|||
339 ELFPVLMHMKP 349

RESULT 11
ADES8179
ID ADE58179 standard; protein; 409 AA.

XX ADE58179;

DT 29-JAN-2004 (first entry)

DE Human Protein P32121, SEQ ID NO 4050.

XX Human; pain; neuronal tissue; gene therapy;

KM spinal segmental nerve injury; chronic constriction injury; CCI;

XX spared nerve injury; SNI; Chung.

OS Homo sapiens.

XX WO2003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

PI Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

DR GENBANK; P32121.

XX New composition comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat

CC or human polynucleotides or a polynucleotide which represents a fragment,

CC derivative or allelic variation of the nucleic acid sequence. Also

CC claimed are a vector comprising the novel polynucleotide, a host cell

CC comprising the vector, a method for identifying a nucleotide sequence

CC which is differentially regulated in an animal subjected to pain and a

CC kit to perform the method, an array, a method for identifying an agent

CC that increases or decreases the expression of the polynucleotide sequence

CC that is differentially expressed in neuronal tissue of a first animal

CC subjected to pain, a method for identifying a compound which regulates

CC the expression of a polynucleotide sequence which is differentially

CC expressed in an animal subjected to pain, a method for identifying a

CC compound that regulates the activity of one or more of the

CC polynucleotides, a method for producing a pharmaceutical composition, a

CC method for identifying a compound or small molecule that regulates the

CC activity in an animal of one or more of the polypeptides given in the

CC specification, a method for identifying a compound useful in treating

CC pain and a pharmaceutical composition comprising the one or more

CC polypeptides or their antibodies. The polynucleotide or the compound that

modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

CC Sequence 409 AA;

Query Match 2.9%; Score 11; DB 7; Length 409;

Best Local Similarity 100.0%; Pred. No. 0.13;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 ELPFVLMHPKP 351

Db 339 ELPFVLMHPKP 349

RESULT 12

ADN95251

ID ADN95251 standard; protein; 409 AA.

AC ADN95251;

DT 01-JUL-2004 (first entry)

DE Human BEC/LBC-related protein sequence SegID173.

growth; differentiation; blood endothelial cell; BEC; lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3; lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cytoskeletal; vasotropic; antiinflammatory; gene therapy; endothelial cell disorder; inflammatory disease; cancer metastasis; lymphatic system; human.

OS Homo sapiens.

PN WO2003080640-A1.

PD 02-OCT-2003.

PF 07-MAR-2003; 2003WO-US006900.

PR 07-MAR-2002; 2002US-0363019P.

PA (LUDM-) LUDMIG INST CANCER RES.

PI (LICN) LICENTIA LTD.

PI Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;

WPI; 2003-876899/81.

DR N-PSDB; ADN95252.

PS Example 1; SEQ ID NO 173; 176pp; English.

This invention relates to a method of differentially modulating the growth or differentiation of blood endothelial cells (BEC) or lymphatic endothelial cells (LEC) comprises contacting endothelial cells with a composition comprising an agent that differentially modulates blood or lymphatic endothelial cells. Treating hereditary lymphoedema comprises identifying a human subject with lymphoedema and with a mutation in at least one allele of a gene encoding a LEC protein, where the mutation correlates with lymphoedema in human subjects, and with the proviso that the LEC protein is not VEGFR-3; and administering to the subject a composition comprising a lymphatic growth agent selected from VEGF-C or VEGF-D polypeptides and polynucleotides. The invention may be useful for the development of compounds with an antiangiogenic, cytoskeletal, vasotropic or antiinflammatory activity or for gene therapy. The method is useful in modulating the growth or differentiation of blood endothelial cells or lymphatic endothelial cells, in treating hereditary lymphoedema, in screening for an endothelial cell disorder or predisposition to the disorder or in monitoring the efficacy or toxicity

of a drug on endothelial cells. The agent is useful in manufacturing a medicament for the differential modulation of blood vessel endothelial cell or lymphatic vessel endothelial cell growth or differentiation. The lymphatic growth agent may also be used in manufacturing a medicament for the treatment of hereditary lymphoedema resulting from a mutation in a LEC gene or of other diseases involving the lymphatic vessels, such as various inflammatory diseases and cancer metastasis via the lymphatic system. The present sequence is that of a human LEC/BEC differentially expressed protein which is related to the method of the invention. Note: This sequence does not appear in the specification but was obtained by the indexer using the source data given in table 14 of the specification.

CC Sequence 409 AA;

Query Match 2.9%; Score 11; DB 7; Length 409;

Best Local Similarity 100.0%; Pred. No. 0.13;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 ELPFVLMHPKP 351

Db 339 ELPFVLMHPKP 349

RESULT 13

ADY15068

ID ADY15068 standard; protein; 409 AA.

AC ADY15068;

DT 05-MAY-2005 (first entry)

DE PRO polypeptide SEQ ID NO 874.

Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive; Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic; Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic; Vincicide; Gastrointestinal-Gen.; Antipsoriatic; Antiaesthetic; Antiallergic; ds; gene; diagnosis.

OS Homo sapiens.

PN WO2005016962-A2.

PD 24-FEB-2005.

PF 11-AUG-2004; 2004WO-US026249.

PR 11-AUG-2003; 2003US-0493546P.

PA (GERTH) GEMENTECH INC.

PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;

WPI; 2005-182330/19.

New nucleic acid encoding PRO polypeptide, useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.

PS Claim 8; SEQ ID NO 874; 158pp; English.

The invention relates to an isolated nucleic acid encoding a PRO polypeptide. The polypeptide, agonist or an antagonist, antibody, composition, and method are useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis. The present sequence represents a DNA encoding a PRO polypeptide.

CC Sequence 409 AA;

Query Match 2.9%; Score 11; DB 9; Length 409;

Best Local Similarity 100.0%; Pred. No. 0.13;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 ELFPVLMHMKP 351
| | | | |
DB 339 ELFPVLMHMKP 349

RESULT 14

ABG69496
ID ABG69496 standard; protein; 410 AA.

XX AC ABG69496;

XX DT 21-OCT-2002 (first entry)

XX DE Rat bait protein beta arrestin 2.

XX KM Rat; yeast two-hybrid assay; adipocyte; bait protein; NIDDM;
XX KM non-insulin diabetes mellitus; obesity; selected interacting domain; SID;
XX KM protein-protein interaction map; PIM; anorectic; metabolic disorder.

XX OS Rattus sp.

XX PN WO200253726-A2.

XX PD 11-JUL-2002.

XX PF 28-DEC-2001; 2001WO-EP0154423.

XX PR 02-JAN-2001; 2001US-0259377P.

XX PA (HYBR-) HYBRIGENICS.

XX PA (CNRS) CENT NAT RECH SCI.

XX PI Legrain P, Marullo S, Jockers R;

XX DR WPI; 2002-583612/62.

XX DR N-PSDB; ABS51032.

XX PT Novel complex of protein-protein interactions in adipocyte cells for
XX PT identifying compounds that modulate the protein-protein interactions and
XX PT useful for treating obesity and metabolic disorders.

XX PS Claim 1; Page 53; 125pp; English.

XX CC The invention relates to a complex of protein-protein interactions
XX CC (forming a protein-protein interaction map, PIM) in adipocyte cells as
XX CC defined in the specification, or polynucleotides in adipocytes encoding
XX CC for the polypeptides. Also included are a recombinant cell expressing the
XX CC interacting polypeptides and a method of selecting a modulating compound
XX CC in adipocyte cells, by cultivating a recombinant host cell on a selective
XX CC medium containing a modulating compound and a reporter gene the
XX CC expression of which is toxic for the recombinant host cell which is
XX CC transformed with two vectors, where the first vector comprises a
XX CC polynucleotide encoding a first hybrid polypeptide and DNA binding domain
XX CC and the second vector comprising a polynucleotide encoding a second
XX CC hybrid polypeptide and an activating domain that activates the toxic
XX CC selecting gene, when the first and second hybrid polypeptides interact and
XX CC selecting the modulating compound which inhibits the growth of the
XX CC recombinant host cell (i.e. using the yeast two-hybrid system). The
XX CC complexes are useful for identifying compounds that modulate the protein-
XX CC protein interactions and useful for treating obesity and metabolic
XX CC disorders e.g. non-insulin dependent diabetes mellitus, NIDDM. The
XX CC compound isolated by the method is useful for treating and preventing
XX CC obesity or metabolic diseases. The interactions between the proteins of
XX CC the complex further define a set of selected interacting domains, SID.
XX CC The present sequence represents a member of the protein complex of the
XX CC invention, used as the bait protein in the yeast two- hybrid assay

XX SQ Sequence 410 AA;

Query Match 2.9%; Score 11; DB 5; Length 410;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 ELFPVLMHMKP 351
| | | | |
DB 340 ELFPVLMHMKP 350

RESULT 15

ADE58177
ID ADE58177 standard; protein; 410 AA.

XX AC ADE58177;

XX DT 29-JAN-2004 (first entry)

XX DE Rat Protein P29067, SEQ ID NO 4048.

XX KM Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX KM chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX OS Rattus norvegicus.

XX PN WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-0333347P.

XX PA (GEHO) GEN HOSPITAL CORP.

XX PA (FARB) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;

XX DR WPI; 2003-268312/26.

XX DR GENBANK; P29067.

XX PT New composition comprising two or more isolated polypeptides, useful for
XX PT preparing a medicament for treating pain in an animal.

XX PS Claim 1; Page; 1017pp; English.

XX CC The invention discloses a composition comprising two or more isolated rat
XX CC or human polynucleotides or a polynucleotide which represents a fragment,
XX CC derivative or allelic variation of the nucleic acid sequence. Also
XX CC claimed are a vector comprising the novel polynucleotide, a host cell
XX CC comprising the vector, a method for identifying a nucleotide sequence
XX CC which is differentially regulated in an animal subjected to pain and a
XX CC kit to perform the method, an array, a method for identifying an agent
XX CC that increases or decreases the expression of the polynucleotide sequence
XX CC that is differentially expressed in neuronal tissue of a first animal
XX CC subjected to pain, a method for identifying a compound which regulates
XX CC the expression of a polynucleotide sequence which is differentially
XX CC expressed in an animal subjected to pain, a method for identifying a
XX CC compound that regulates the activity of one or more of the
XX CC polynucleotides, a method for producing a pharmaceutical composition, a
XX CC method for identifying a compound or small molecule that regulates the
XX CC activity in an animal of one or more of the polypeptides given in the
XX CC specification, a method for identifying a compound useful in treating
XX CC pain and a pharmaceutical composition comprising the one or more
XX CC polypeptides or their antibodies. The polynucleotide or the compound that
XX CC modulates its activity is useful for preparing a medicament for treating
XX CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX CC therapy). The sequence presented is a rat protein (shown in Table 2 of
XX CC the specification) which is differentially expressed during pain. Note:
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic form directly from WIPO at
XX CC ftp.wipo.int/pub/published_ptc_sequences.

XX SQ Sequence 410 AA;

Query Match 2.9%; Score 11; DB 7; Length 410;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 341 ELPPVLMHMKP 351
 |||||
 Db 340 ELPPVLMHMKP 350

Search completed: May 20, 2006, 23:10:23
 Job time : 198 secs

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OM protein - protein search, using sw model

Run on: May 20, 2006, 23:10:44 ; Search time 40 Seconds
(without alignments)
921.276 Million cell updates/sec

Title: US-10-056-405-2

Perfect score: 383

Sequence: 1 MVTNFKVFKKCAPNGKVTLY.....ADVTFRQDTIDQASVDFE 383

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size: 1

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :
1: pirl:*
2: pirl:*
3: pirl:*
4: pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	5.2	364	2	A34867
2	17	4.4	363	2	A55081
3	16	4.2	381	2	B56607
4	12	3.1	407	2	A56607
5	11	2.9	401	2	A34856
6	11	2.9	401	2	S11566
7	11	2.9	401	2	B55081
8	11	2.9	405	2	S68254
9	11	2.9	407	2	S68253
10	11	2.9	409	2	S18984
11	11	2.9	410	2	A59279
12	11	2.9	415	2	S68255
13	11	2.9	420	2	A47140
14	11	2.9	387	2	I55423
15	9	2.3	388	2	S38943
16	9	2.3	1773	2	T05128
17	8	2.1	403	2	US0066
18	8	2.1	403	2	S03960
19	8	2.1	404	2	A28404
20	8	2.1	405	2	A30357
21	8	2.1	412	2	F87709
22	8	2.1	418	2	B46682
23	8	2.1	418	2	A34851
24	8	2.1	418	2	B43404
25	8	2.1	448	2	D71852
26	8	2.1	448	2	H64663
27	7	1.8	53	2	AF2764
28	7	1.8	57	2	PT0202
29	7	1.8	63	1	MSWML5

30	7	1.8	92	2	B82603	hypothetical prote
31	7	1.8	111	2	S10222	hypothetical prote
32	7	1.8	139	2	E97426	flagellar basal-bo
33	7	1.8	139	2	AE2644	flagellar basal-bo
34	7	1.8	142	2	F81048	conserved hypothet
35	7	1.8	145	2	C64447	hypothetical prote
36	7	1.8	149	2	A87346	hypothetical prote
37	7	1.8	151	2	A83639	osmotically induci
38	7	1.8	155	2	C81827	hypothetical prote
39	7	1.8	161	2	A27873	allophycocyanin al
40	7	1.8	166	2	A95969	hypothetical prote
41	7	1.8	174	2	S39877	carQ protein - Myx
42	7	1.8	216	2	A61259	glycoprotein S - p
43	7	1.8	217	2	B64080	hypothetical prote
44	7	1.8	231	2	S73469	probable lipoprote
45	7	1.8	231	2	A62084	MTR/SMH nucleosida

ALIGNMENTS

RESULT 1
A34867
arrestin - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 09-Jul-2004
C:Accession: A34867; A34868
R:Smith, D.P.; Shieh, B.H.; Zuker, C.S.
Proc. Natl. Acad. Sci. U.S.A. 87, 1003-1007, 1990
A:Title: Isolation and structure of an arrestin gene from Drosophila.
A:Reference number: A34867; MUID:90138925; PMID:1689056
A:Accession: A34867
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-364 <SMI>
A:Cross-references: UNIPROT:P15372; UNIPARC:UPI0000000569; GB:M30177
R:Hyde, D.R.; Mecklenburg, K.L.; Pollock, J.A.; Vitellie, T.S.; Benzer, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 1008-1012, 1990
A:Title: Twenty Drosophila visual system cDNA clones: one is a homolog of human arrestin
A:Reference number: A34868; MUID:90138926; PMID:2105491
A:Accession: A34868
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-364 <HYD>
A:Cross-references: UNIPARC:UPI0000000569; GB:M30140; NID:G156961; PIDN:AAA28380.1; PID:
C:Genetics:
A:Gene: FlyBase:Arr1
A:Cross-references: FlyBase:FBgn0000120
A:Introns: 36/3; 306/3; 349/3
C:Superfamily: arrestin

Query Match 5.2%; Score 20; DB 2; Length 364;
Best Local Similarity 100.0%; Pred. No. 3.2e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 VKKIKAMVQGVVFLFQNG 247
DB 227 VKKIKAMVQGVVFLFQNG 246

RESULT 2
A55081
arrestin 1 - bluebottle fly (Calliphora vicina)
C:Species: Calliphora vicina
C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C:Accession: A55081; S44291
R:Plangger, A.; Mallick, D.; Whitney, M.; Paulsen, R.
J. Biol. Chem. 269, 26969-26975, 1994
A:Title: Mechanism of arrestin 2 function in rhodometric photoreceptors.
A:Reference number: A55081; MUID:95014564; PMID:7929436
A:Accession: A55081
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-363 <PIA>
A:Cross-references: UNIPROT:P51486; UNIPARC:UPI0000126075; GB:X79072; NID:g483527; PIDN:
A>Note: the source is designated as Calliphora erythrocephala
C:Superfamily: arrestin

Query Match 4.4%; Score 17; DB 2; Length 363;
Best Local Similarity 100.0%; Pred. No. 4e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 322 SYAVKVKLFGLGAGEL 338
|||
Db 321 SYAVKVKLFGLGAGEL 337

RESULT 3

B56607
arrestin homolog - tobacco budworm
C:Species: Heliothis virescens (tobacco budworm)
C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
C:Accession: B56607
R:Ramirez, K.; Freitag, J.; Krieger, J.; Breer, H.
Cell. Signal. 5, 69-80, 1993
A:Title: Arrestin-subtypes in insect antennae.
A:Reference number: A56607; MUID:9319955; PMID:8452755
A:Accession: B56607
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tree
A:Molecule type: mRNA
A:Residues: 1-381 <RAM>
A:Cross-references: UNIPROT:P55274; UNIPARC:UPI0000126089
A:Experimental source: antennae
A>Note: sequence extracted from NCBI backbone (NCBI:P127926)
C:Superfamily: arrestin

Query Match 4.2%; Score 16; DB 2; Length 381;
Best Local Similarity 100.0%; Pred. No. 4.5e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYVNFVKFKKCAPNGK 16
|||
Db 1 MYVNFVKFKKCAPNGK 16

RESULT 4

A56607
arrestin homolog - migratory locust
C:Species: Locusta migratoria (migratory locust)
C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
C:Accession: A56607
R:Ramirez, K.; Freitag, J.; Krieger, J.; Breer, H.
Cell. Signal. 5, 69-80, 1993
A:Title: Arrestin-subtypes in insect antennae.
A:Reference number: A56607; MUID:9319955; PMID:8452755
A:Accession: A56607
A:Contents: antennae
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-407 <RAM>
A:Cross-references: UNIPROT:P32122; UNIPARC:UPI0000126088; GB:S57174; NID:g298755; PIDN:
A>Note: sequence extracted from NCBI backbone (NCBI:N127923; NCBI:P127925)
C:Superfamily: arrestin

Query Match 3.1%; Score 12; DB 2; Length 407;
Best Local Similarity 100.0%; Pred. No. 0.00064;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 62 RYGRDEDEVMG 73
|||
Db 69 RYGRDEDEVMG 80

RESULT 5

A34856
49k photoreceptor protein - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 09-Jul-2004
C:Accession: A34856
R:Ramada, T.; Takeuchi, Y.; Komori, N.; Kobayashi, H.; Sakai, Y.; Hotta, Y.; Matsumoto, T.
Science 248, 483-485, 1990
A:Title: A 49-kilodalton phosphoprotein in the Drosophila photoreceptor is an arrestin homolog.
A:Reference number: A34856; MUID:90232360; PMID:2158671
A:Accession: A34856
A:Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-401 <YAM>
A:Cross-references: UNIPROT:P19107; UNIPARC:UPI0000126081; GB:M52141; NID:g158157; PIDN:
A:Gene: FlyBase:Arr2
A:Cross-references: FlyBase:FBgn0000121
C:Superfamily: arrestin

Query Match 2.9%; Score 11; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 62 RYGRDEDEVMG 72
|||
Db 61 RYGRDEDEVMG 71

RESULT 6

S11566
arrestin homolog - fruit fly (Drosophila miranda)
C:Species: Drosophila miranda
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S11566
R:Krishnan, R.; Ganguly, R.
Nucleic Acids Res. 19, 5894, 1990
A:Title: Nucleotide sequence of the arrestin-like 49 kD protein gene of Drosophila miranda.
A:Reference number: S11566; MUID:9101944; PMID:2216789
A:Accession: S11566
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-401 <KRI>
A:Cross-references: UNIPROT:P19108; UNIPARC:UPI0000126082; EMBL:X54084; NID:g7612; PIDN:
C:Gene: FlyBase:Dmir/Arr2
A:Cross-references: FlyBase:FBgn0012552
A:Introns: 286/1; 351/1
C:Superfamily: arrestin

Query Match 2.9%; Score 11; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 62 RYGRDEDEVMG 72
|||
Db 61 RYGRDEDEVMG 71

RESULT 7

B55081
arrestin 2 - bluebotle fly (Calliphora vicina)
C:Species: Calliphora vicina
C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C:Accession: B55081; S44292
R:Plangger, A.; Malicki, D.; Whitney, M.; Paulsen, R.
J. Biol. Chem. 269, 26960-26975, 1994
A:Title: Mechanism of arrestin 2 function in rhododermic photoreceptors.
A:Reference number: A55081; MUID:95014564; PMID:7929436
A:Accession: B55081
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-401 <PIA>
A:Cross-references: UNIPROT:P51487; UNIPARC:UPI00001688DC; EMBL:X79073; NID:g483583; PIDN:
A>Note: the source is designated as Calliphora erythrocephala
C:Superfamily: arrestin

Query Match 2.9%; Score 11; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 62 RYGREDEVMG 72
|||||
Db 61 RYGREDEVMG 71

RESULT 8

S68254
arrestin isoform 2S, erythrocyte - rainbow trout
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S68254
R:Jahns, R.; Borgese, F.; Lindenthal, S.; Straub, A.; Motals, R.; Fievel, B.
Biochem. J. 316, 497-506, 1996
A:Title: Trout red blood cell arrestin (TRCarr), a novel member of the arrestin family:
A:Reference number: S68253; MUID:96257743; PMID:8687393
A:Accession: S68254
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-405 <JAH>
A:Cross-references: UNIPROT:P51467; UNIPARC:UPI000012607C; GB:U48410
C:Superfamily: arrestin

Query Match 2.9%; Score 11; DB 2; Length 405;
Best Local Similarity 100.0%; Pred. No. 0.0069;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 341 ELFPVLMHMKP 351
|||||
Db 339 ELFPVLMHMKP 349

RESULT 9

S68253
arrestin isoform 1S, erythrocyte - rainbow trout
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S68253
R:Jahns, R.; Borgese, F.; Lindenthal, S.; Straub, A.; Motals, R.; Fievel, B.
Biochem. J. 316, 497-506, 1996
A:Title: Trout red blood cell arrestin (TRCarr), a novel member of the arrestin family:
A:Reference number: S68253; MUID:96257743; PMID:8687393
A:Accession: S68253
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-407 <JAH>
A:Cross-references: UNIPROT:P51466; UNIPARC:UPI0000126077; GB:U48410; NID:91215723; PIDN
C:Superfamily: arrestin

Query Match 2.9%; Score 11; DB 2; Length 407;
Best Local Similarity 100.0%; Pred. No. 0.0069;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 341 ELFPVLMHMKP 351
|||||
Db 339 ELFPVLMHMKP 349

RESULT 10

S18984
arrestin - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S18984
R:Rapoport, B.
submitted to the EMBL Data Library, November 1991
A:Description: Isolation of a novel cDNA belonging to the arrestin family from human thymocytes
A:Reference number: S18984
A:Accession: S18984

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-409 <RAP>
A:Cross-references: UNIPROT:P31211; UNIPARC:UPI000016458B; EMBL:Z11501; NID:928850; PIDN
C:Superfamily: arrestin

Query Match 2.9%; Score 11; DB 2; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 341 ELFPVLMHMKP 351
|||||
Db 339 ELFPVLMHMKP 349

RESULT 11

A59279
beta-arrestin 2 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C:Accession: A59279; A43404; I70112
R:Altman, H.; Ariz, J.L.; Aoki, C.; Dawson, T.M.; Codina, J.; Kwatra, M.M.; Snyder
submitted to GenBank, August 1995
A:Reference number: A59279
A:Accession: A59279
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-410 <ATT>
A:Cross-references: UNIPROT:P29067; UNIPARC:UPI000012607D; GB:M91590; NID:949986; PIDN:
A:Experimental source: strain Sprague-Dawley; stage adult; tissue type brain; tissue lib
R:Altman, H.; Ariz, J.L.; Aoki, C.; Dawson, T.M.; Codina, J.; Kwatra, M.M.; Snyder
J. Biol. Chem. 267, 17882-17890, 1992
A:Title: Beta-arrestin2, a novel member of the arrestin/beta-arrestin gene family.
A:Reference number: A43404; MUID:92386146; PMID:1517224
A:Accession: A43404
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-320, 'A', 322-325, 'A', 327-330, 'A', 332-410 <ATG>
A:Cross-references: UNIPARC:UPI00001788C; GB:M91590; NID:949986
A:Note: sequence extracted from NCBI backbone (NCBI:112790)
A:Note: the sequence is revised in GenBank entry RATTBARRS2, release 113.0
J. Biol. Chem. 269, 4613-4619, 1994
A:Title: Cone arrestin identified by targeting expression of a functional family.
A:Reference number: 155423; MUID:94140898; PMID:8308033
A:Accession: 170112
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 295-410 <CRA>
A:Cross-references: UNIPARC:UPI0000170BB4; EMBL:U03627; NID:9458202; PIDN:AAA17551.1; PI
C:Superfamily: arrestin

Query Match 2.9%; Score 11; DB 2; Length 410;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 341 ELFPVLMHMKP 351
|||||
Db 340 ELFPVLMHMKP 350

RESULT 12

S68255
arrestin isoform 1L, erythrocyte - rainbow trout
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S68255
R:Jahns, R.; Borgese, F.; Lindenthal, S.; Straub, A.; Motals, R.; Fievel, B.
Biochem. J. 316, 497-506, 1996
A:Title: Trout red blood cell arrestin (TRCarr), a novel member of the arrestin family:
A:Reference number: S68253; MUID:96257743; PMID:8687393
A:Accession: S68255
A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA
A:Residues: 1-415 <JAH>
A:Cross-references: UNIPROT:P51468; UNIPARC:UPI000012607E; GB:U48410
C:Superfamily: arrestin

Query Match 2.9%; Score 11; DB 2; Length 415;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 341 ELPFVLMHMKP 351
|||
DB 347 ELPFVLMHMKP 357

RESULT 13

A47140
arrestin arr3L - bovine
N:Contains: arrestin arr3S
C:Species: Bos primigenius taurus (cattle)
C:Date: 16-Feb-1994 #sequence revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: A47140; B47140; U2051
R:Stearns-Marr, R.; Gurevich, V.V.; Goldsmith, P.; Bodine, R.C.; Sanders, C.; Donoso, L.A.
J. Biol. Chem. 268, 15640-15648, 1993
A:Title: Polypeptide variants of beta-arrestin and arrestin3.
A:Reference number: A47140; MUID:93340166; PMID:8340388
A:Accession: A47140
A:Molecule type: mRNA
A:Residues: 1-420 <ST>
A:Cross-references: UNIPROT:P32120; UNIPARC:UPI0000178BC2; GB:L14641
A:Experimental source: brain
A:Note: sequence extracted from NCBI backbone (NCBIN:136006, NCBI:P:136007)
A:Accession: B47140
A:Molecule type: mRNA
A:Residues: 1-362,374-420 <ST2>
A:Cross-references: UNIPARC:UPI0000178BC3
C:Comment: This protein plays a role in the regulation of G-protein-coupled receptors.
C:Superfamily: arrestin
F:1-420/Product: arrestin arr3L #status predicted <MAT>
F:1-362,374-420/Product: arrestin arr3S #status predicted <MA2>

Query Match 2.9%; Score 11; DB 2; Length 420;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 341 ELPFVLMHMKP 351
|||
DB 339 ELPFVLMHMKP 349

RESULT 14

I55423
arrestin-C - human
C:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 13-Sep-1998
C:Accession: I55423
R:Craft, C.M.; Whitmore, D.H.; Wiechmann, A.F.
J. Biol. Chem. 269, 4613-4619, 1994
A:Title: Cone arrestin identified by targeting expression of a functional family.
A:Reference number: I55423; MUID:94140898; PMID:8308033
A:Accession: I55423
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-387 <RES>
A:Cross-references: UNIPARC:UPI0000178BC4; EMBL:U03626; NID:g458200; PID:g458201
C:Superfamily: arrestin

Query Match 2.3%; Score 9; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 0.77;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 GKRDVVDHV 30
|||
DB 19 GKRDVVDHV 27

RESULT 15

S38943
arrestin - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C:Accession: S38943
R:Murakami, A.; Yajima, T.; Sakuma, H.; McLaren, M.J.; Inana, G.
FEBS Lett. 334, 203-209, 1993
A:Title: X-arrestin: a new retinal arrestin mapping to the X chromosome.
A:Reference number: S38943; MUID:94039835; PMID:8224247
A:Accession: S38943
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-388 <MR>
A:Cross-references: UNIPROT:P36575; UNIPARC:UPI000004230C; GB:S66793; NID:g439830; PIDN:7
C:Superfamily: arrestin

Query Match 2.3%; Score 9; DB 2; Length 388;
Best Local Similarity 100.0%; Pred. No. 0.77;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 GKRDVVDHV 30
|||
DB 19 GKRDVVDHV 27

Search completed: May 20, 2006, 23:16:16
Job time : 42 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 20, 2006, 23:07:08 ; Search time 301 Seconds
(without alignments)
1177.013 Million cell updates/sec

Title: US-10-056-405-2
Perfect score: 383
Sequence: 1 MYNFKVFKKCAPNGKVTLY.....ADVFETPRODTIDQASVDFE 383

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2849598 seqs, 925015592 residues

Word size: 1
Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: UniProt 7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of residues predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	383	100.0	383	Q7PMG5	anopheles g
2	383	100.0	383	Q95NF3	anopheles g
3	245	64.0	245	Q6VPO0	anopheles g
4	233	60.8	269	Q5TNM2	anopheles g
5	25	6.5	381	Q9B1G9	anopheles g
6	20	5.2	364	ARRA_DROME	anopheles g
7	18	4.7	18	Q7YTV9	anopheles g
8	18	4.7	18	Q7YTV9	anopheles g
9	18	4.7	18	Q7YTV9	anopheles g
10	17	4.4	363	ARR1_CALVI	anopheles a
11	16	4.2	381	ARRH_HEIVI	anopheles v
12	14	3.7	52	Q6X1Z6	anopheles v
13	13	3.4	400	ARRH_LIMPO	anopheles pol
14	12	3.1	407	ARRH_LOCT1	anopheles m
15	12	2.9	217	Q68DZ5	anopheles m
16	11	2.9	390	Q5B1J0	anopheles a
17	11	2.9	390	Q5B1J0	anopheles a
18	11	2.9	398	Q70508	anopheles g
19	11	2.9	400	ARRB_CALVI	anopheles g
20	11	2.9	401	ARRB_DROME	anopheles g
21	11	2.9	402	ARRB_DROME	anopheles g
22	11	2.9	405	Q3TRC8	anopheles m
23	11	2.9	406	Q5F2D9	anopheles m
24	11	2.9	406	Q5F2D9	anopheles m
25	11	2.9	407	ARR1_ONCMY	anopheles m
26	11	2.9	408	Q6DFC4	anopheles m
27	11	2.9	408	Q6DFY2	anopheles m
28	11	2.9	408	Q7T2D2	anopheles m
29	11	2.9	409	ARRB2_HUMAN	anopheles m
30	11	2.9	409	Q2P1J5	anopheles m
31	11	2.9	409	Q61CT3	anopheles m

32	11	2.9	409	Q5RCR4	pongo pygma
33	11	2.9	410	ARRB2_MOUSE	mus musculus
34	11	2.9	410	ARRB2_RAT	rattus norv
35	11	2.9	410	Q59EM5	homo sapien
36	11	2.9	410	Q3TCM2	mus musculus
37	11	2.9	410	Q5F2E0	mus musculus
38	11	2.9	415	ARR3_ONCMY	oncorhynch
39	11	2.9	420	ARR3_BOVIN	bos taurus
40	11	2.9	421	Q5F2D8	mus musculus
41	10	2.6	147	Q6WGR2	metapenaeus
42	10	2.6	176	Q4V8R0	brachydanio
43	10	2.6	386	Q4SPF4	tetradodon n
44	9	2.3	157	Q5XJ55	brachydanio
45	9	2.3	359	Q5J723	homo sapien

ALIGNMENTS

RESULT 1
Q7PMG5 ANOGA PRELIMINARY; PRT; 383 AA.
AC Q7PMG5;
DT 15-DEC-2003, integrated into UniProtKB/TREMBL.
DT 07-DEC-2004, sequence version 2.
DT 07-FEB-2006, entry version 12.
DE ENSANGP0000012569.
GN ORFNames=ENSANGG0000010080;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation";
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
RL -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.

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EMBL: AAB01008980; EAL13874.3; -; Genomic DNA.
GO: GO:0007600; P: sensory perception; IEA.
GO: GO:0007165; P: signal transduction; IEA.
DR InterPro: IPR006698; Arrestin.
DR InterPro: IPR011021; Arrestin_C.
DR InterPro: IPR011021; Arrestin_N.
DR PANTHER: PTHR11792; Arrestin; 1.
DR Pfam: PF02752; Arrestin_C; 1.
DR Pfam: PF00339; Arrestin_N; 1.
DR PRINTS: PR00309; ARRESTIN.
DR ProDom: PD002099; Arrestin; 2.
DR PROSITE: PS00295; ARRESTINS; 1.
SQ SEQUENCE 383 AA; 42809 MW; FA946438592BB53E CRC64;

Query Match 100.0%; Score 383; DB 2; Length 383;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNFKVFKKCAPNGKVTLYNGKRDVVDHVGVEPIDIVLDDFYINDNRKVFQIYCS 60
DB 1 MYNFKVFKKCAPNGKVTLYNGKRDVVDHVGVEPIDIVLDDFYINDNRKVFQIYCS 60

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QY 61 FRYREDEWVGLNFQKELCLASBOIYPRPEKSDKEQTKLOERLLKKGNSNAIPEFTNIS 120
DB 61 FRYREDEWVGLNFQKELCLASBOIYPRPEKSDKEQTKLOERLLKKGNSNAIPEFTNIS 120
QY 121 PNASSVTLQOGEDDNGPCGVSYVVKIFAGESETDTRHRSYVTLGIRKIQFAPTKQG 180
DB 121 PNASSVTLQOGEDDNGPCGVSYVVKIFAGESETDTRHRSYVTLGIRKIQFAPTKQG 180
QY 181 OPTLVKRDPMFLSPGEELEVTLDKQYLHGERIGVNICIRNNSNKWVKIKAMVQOGVD 240
DB 181 OPTLVKRDPMFLSPGEELEVTLDKQYLHGERIGVNICIRNNSNKWVKIKAMVQOGVD 240
QY 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKQRRGIALDGOIKRQDQ 300
DB 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKQRRGIALDGOIKRQDQ 300
QY 301 CLASTTLLAQPDPQDAGCVIISYAVKVLFLGALGELSLELPVLVMPKPGTAKVITHA 360
DB 301 CLASTTLLAQPDPQDAGCVIISYAVKVLFLGALGELSLELPVLVMPKPGTAKVITHA 360
QY 361 DSOADVETFRDPTIDQOASVDPE 383
DB 361 DSOADVETFRDPTIDQOASVDPE 383

RESULT 2
ID 06VPP0_ANOGA PRELIMINARY: PRT: 383 AA.
AC 06VPP0;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE Arrestin.
GN Name=Arct1.
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_Taxid=7165;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Antennae, and Head;
RX MEDLINE=21680430, PubMed=11822731, DOI=10.1007/s00436-002-0637-0;
RA Ricci I., Santolamazza F., Costantini C., Favia G.;
RT "Molecular characterization and chromosomal mapping of transcripts
RT having tissue-specific expression in the malaria mosquito anopheles
RT gambiae: possible involvement in visual or olfactory processes.";
RL Parasitol. Res. 88:1-8(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G3;
RX MEDLINE=21819361, PubMed=11792843, DOI=10.1073/pnas.022505499;
RA Merrill C.E., Riesgo-Escovar J., Pitter R.J., Kafatos F.C.;
RT "Visual arrestin in olfactory pathways of Drosophila and the malaria
RT vector mosquito Anopheles gambiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:1633-1638(2002).
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CC
EMBL: AJ304409; CAC39103.2; -; mRNA.
EMBL: AY017417; AAC54081.1; -; mRNA.
HSSP: P17870; 1G4M.
DR Ensembl, ENSANGG00000010080; Anopheles gambiae.
DR GO: GO:0007600; P:sensory perception; IEA.
DR GO: GO:0007165; P:signal transduction; IEA.
DR InterPro: IPR000698; Arrestin.
DR InterPro: IPR011022; Arrestin_C.
DR InterPro: IPR011021; Arrestin_N.
DR PANTHER: PTHR11792; Arrestin; 1.
DR Pfam: PF02752; Arrestin_C; 1.
DR Pfam: PF02752; Arrestin_N; 1.
```

```
DR PRINTS: PR00309; ARRESTIN.
DR PROSITE: PS00295; ARRESTIN; 1. FA946438592BB53E CRC64;
SQ SEQUENCE 383 AA; 42809 MW; 1.
Query Match 100.0%; Score 383; DB 2; Length 383;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVVNFKFKKCAPRGKVTLMGKRDPVDHVSQVPEPIDGIWLDDEYIRDNKKYFGQIVCS 60
DB 1 MVVNFKFKKCAPRGKVTLMGKRDPVDHVSQVPEPIDGIWLDDEYIRDNKKYFGQIVCS 60
QY 61 FRYREDEWVGLNFQKELCLASBOIYPRPEKSDKEQTKLOERLLKKGNSNAIPEFTNIS 120
DB 61 FRYREDEWVGLNFQKELCLASBOIYPRPEKSDKEQTKLOERLLKKGNSNAIPEFTNIS 120
QY 121 PNASSVTLQOGEDDNGPCGVSYVVKIFAGESETDTRHRSYVTLGIRKIQFAPTKQG 180
DB 121 PNASSVTLQOGEDDNGPCGVSYVVKIFAGESETDTRHRSYVTLGIRKIQFAPTKQG 180
QY 181 OPTLVKRDPMFLSPGEELEVTLDKQYLHGERIGVNICIRNNSNKWVKIKAMVQOGVD 240
DB 181 OPTLVKRDPMFLSPGEELEVTLDKQYLHGERIGVNICIRNNSNKWVKIKAMVQOGVD 240
QY 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKQRRGIALDGOIKRQDQ 300
DB 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKQRRGIALDGOIKRQDQ 300
QY 301 CLASTTLLAQPDPQDAGCVIISYAVKVLFLGALGELSLELPVLVMPKPGTAKVITHA 360
DB 301 CLASTTLLAQPDPQDAGCVIISYAVKVLFLGALGELSLELPVLVMPKPGTAKVITHA 360
QY 361 DSOADVETFRDPTIDQOASVDPE 383
DB 361 DSOADVETFRDPTIDQOASVDPE 383

RESULT 3
ID 06VPP0_ANOGA PRELIMINARY: PRT: 245 AA.
AC 06VPP0;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Arrestin (Fragment).
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_Taxid=7165;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=4ARR, Yaounde, and L3-5;
RA Wolras 1., Poncon N., Simard F., Cohuet A., Fontenille D.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
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CC
EMBL: AY333991; AAR01116.1; -; Genomic DNA.
EMBL: AY333992; AAR01117.1; -; Genomic DNA.
EMBL: AY333993; AAR01118.1; -; Genomic DNA.
EMBL: AY333995; AAR01120.1; -; Genomic DNA.
EMBL: AY333996; AAR01121.1; -; Genomic DNA.
EMBL: AY333994; AAR01119.1; -; Genomic DNA.
HSSP: P08168; 1AYR.
DR GO: GO:0007600; P:sensory perception; IEA.
DR GO: GO:0007165; P:signal transduction; IEA.
DR InterPro: IPR000698; Arrestin.
DR InterPro: IPR011022; Arrestin_C.
DR PANTHER: PTHR11792; Arrestin; 1.
DR Pfam: PF02752; Arrestin_C; 1.
```

DR PRINTS; PR00309; ARRESTIN.
 DR Prodom; PD002099; Arrestin; 2.
 FT NON_TER 1
 FT NON_TER 245
 SQ SEQUENCE 245 AA; 27038 MW; 86DBF4520115DASF CRC64;

Query Match 64.0%; Score 245; DB 2; Length 245;
 Best Local Similarity 100.0%; Pred. No. 1.9e-236;
 Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 LQGGEDNDGDCGVSYYVKIFAGESEDTDRTRRSTVTLGIRKIQFAPTKQGOCTLVK 188
 DB 1 LQGGEDNDGDCGVSYYVKIFAGESEDTDRTRRSTVTLGIRKIQFAPTKQGOCTLVK 60
 QY 189 DFMISPELELEVTLDKQLYLHGERIGVNICIRNNSNMKVKKIKAMVQGVVYLFQNGS 248
 DB 61 DFMISPELELEVTLDKQLYLHGERIGVNICIRNNSNMKVKKIKAMVQGVVYLFQNGS 120
 QY 249 YRNTVASLETSEGCPIQPGSSLOKVMYLTPLISSNKGRIALDQIKRQDCLASTLL 308
 DB 121 YRNTVASLETSEGCPIQPGSSLOKVMYLTPLISSNKGRIALDQIKRQDCLASTLL 180
 QY 309 AQPORDAFGVITSAVKVFLFGALGELSALPFLMHPKPGTKAKVIHADSOADYET 368
 DB 181 AQPORDAFGVITSAVKVFLFGALGELSALPFLMHPKPGTKAKVIHADSOADYET 240
 QY 369 FRODT 373
 DB 241 FRODT 245

RESULT 4

OSTNM2 ANOGA PRELIMINARY; PRT; 269 AA.

AC 05TNW2
 DT 07-DEC-2004, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 1.
 DE ENSANGP0000027511 (Fragment).
 GN ORFNames=ENSANG0000010080;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
 OC Anophelinae; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RT "Anopheles gambiae re-annotation."
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RT Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
 RL -! CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.

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 CC -----
 DR EMBL; AAA801008980; EAL39278.1; -; Genomic DNA.
 DR GO; GO:0007600; P:sensory perception; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000698; Arrestin.
 DR InterPro; IPR011022; Arrestin_C.
 DR InterPro; IPR011021; Arrestin_N.
 DR PANTHER; PTHR11792; Arrestin_1.
 DR Pfam; PF02752; Arrestin_C; 1.
 DR Pfam; PF00339; Arrestin_N; 1.
 DR PRINTS; PR00309; ARRESTIN.

DR Prodom; PD002099; Arrestin; 2.
 DR PROSITE; PS00295; ARRESTINS; 1.
 FT NON_TER 1
 FT NON_TER 269
 SQ SEQUENCE 269 AA; 30553 MW; D45300A28A74F4C0 CRC64;

Query Match 60.8%; Score 233; DB 2; Length 269;
 Best Local Similarity 100.0%; Pred. No. 1.9e-224;
 Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVNFKVFKKCAPKQKTVLYMGRKDFVDHVSVEPIDGIYVLDEYIRDNKRVGQIVCS 60
 DB 37 MVNFKVFKKCAPKQKTVLYMGRKDFVDHVSVEPIDGIYVLDEYIRDNKRVGQIVCS 96
 QY 61 FRYGREDEVMGLNFQKELCLASFOIYPPREKSKQETKIOERLLKLGSAIIPFTNIS 120
 DB 97 FRYGREDEVMGLNFQKELCLASFOIYPPREKSKQETKIOERLLKLGSAIIPFTNIS 156
 QY 121 PNASSVTLQGGEDNDGDCGVSYYVKIFAGESEDTDRTRRSTVTLGIRKIQFAPTKQGO 180
 DB 157 PNASSVTLQGGEDNDGDCGVSYYVKIFAGESEDTDRTRRSTVTLGIRKIQFAPTKQGO 216
 QY 181 QPCTLVKRDPMISPELELEVTLDKQLYLHGERIGVNICIRNNSNMKVKKIKA 233
 DB 217 QPCTLVKRDPMISPELELEVTLDKQLYLHGERIGVNICIRNNSNMKVKKIKA 269

RESULT 5

Q9BIG9 9NEOP PRELIMINARY; PRT; 381 AA.

AC 09BIG9
 DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2001, sequence version 1.
 DT 07-FEB-2006, entry version 17.
 DE Arrestin.
 GN Name=ar1;
 OS Ascalaphus macaronius.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Neuroptera; Ascalaphidae; Ascalaphus.
 OX NCBI_TaxID=146496;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC Tissue=Head;
 RC MEDLINE=21184354; PubMed=11287006; DOI=10.1016/S0014-5793(01)02287-6;
 RA Bentrop J., Schillo M., Gerdon G., Draaijer G., Paulsen R.;
 RT "UV-light-dependent binding of a visual arrestin 1 isoform to
 RT photoreceptor membranes in a neuropteran (Ascalaphus) compound eye."
 RL FEBS Lett. 493:112-116(2001).

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DR EMBL; AJ303080; CAC36938.1; -; mRNA.
 DR HSSP; P17870; 1G4M.
 DR GO; GO:0007600; P:sensory perception; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000698; Arrestin.
 DR InterPro; IPR011022; Arrestin_C.
 DR InterPro; IPR011021; Arrestin_N.
 DR PANTHER; PTHR11792; Arrestin_1.
 DR Pfam; PF02752; Arrestin_C; 1.
 DR Pfam; PF00339; Arrestin_N; 1.
 DR PRINTS; PR00309; ARRESTIN.
 DR PROSITE; PS00295; ARRESTINS; 1.
 SQ SEQUENCE 381 AA; 42789 MW; 451DEB465969857D CRC64;

Query Match 6.5%; Score 25; DB 2; Length 381;
 Best Local Similarity 100.0%; Pred. No. 1e-15;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 RKVFGQIVCSFRYGREDEVMGLNF 75
 DB 52 RKVFGQIVCSFRYGREDEVMGLNF 76

RESULT 6
 ARRA_DROME STANDARD; PRT; 364 AA.
 ID ARRA_DROME; Q9VJ48;
 AC P15372; Q9VJ48;
 DT 01-APR-1990, integrated into UniProtKB/Swiss-Prot.
 DT 01-APR-1990, sequence version 1.
 DT 07-FEB-2006, entry version 58.
 DE Phosrestin-2 (Phosrestin II) (Arrestin A) (Arrestin-1).
 GN Name=Arr1; Synonyms=ArrA, ORFNames=CG5711;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE AND TISSUE SPECIFICITY.
 RX MEDLINE=90138925; PubMed=1689056;
 RA Smith D.P., Sheeh B.-H., Zuker C.S.;
 RT "Isolation and structure of an arrestin gene from Drosophila.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:1003-1007(1990).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=90138926; PubMed=2105491;
 RA Hyde D.R., Mecklenburg K.L., Pollock J.A., Vithelec T.S., Benzer S.;
 RT "Twenty Drosophila visual system cDNA clones: one is a homolog of human arrestin.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:1008-1012(1990).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.-H.C., Blake J.R.G., Champs C.R., McKus G.L.G.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miller D.,
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
 RA Ballew R.M., Baou A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Butkova D., Botchan M.A., Bouck J., Brokstein P., Brothier P.,
 RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,
 RA Foaier C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hootin D., Houston K.A., Howland T.J., Mei M.-H., Ibbagwan C.,
 RA Jaitai M., Kailuen F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mateti B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
 RA Palazzolo M., Plittman G.S., Pan S., Pollard J., Puri V., Rehen M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shie B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strung R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinrock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [4]
 RP GENOME REANNOTATION.

RX MEDLINE=22426069; PubMed=12537572;
 RA Miara S., Crosby M.A., Mungall C.J., Mathews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bernan B.P.,
 RA Bettencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=Berkley; TISSUE=Head;
 RX MEDLINE=22426066; PubMed=12537569;
 RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champs M.,
 RA George R.A., Guarin H., Krommiller B., Paclet J.M., Park S., Man K.H.,
 RA Rubin G.M., Celisner S.E.;
 RT "A Drosophila full-length cDNA resource.";
 RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
 RN [6]
 RP PHOSPHORYLATION.
 RX MEDLINE=91282780; PubMed=1905538;
 RA Matsunoto H., Yamada T.;
 RT "Phosrestins I and II: arrestin homologs which undergo differential light-induced phosphorylation in the Drosophila photoreceptor in vivo.";
 RL Biochem. Biophys. Res. Commun. 177:1306-1312(1991).
 RN [7]
 RP FUNCTION.
 RX MEDLINE=93303590; PubMed=8316831;
 RA Dolph P.J., Ranganathan R., Colley N.J., Hardy R.W., Socolich M.,
 RA Zuker C.S.;
 RT "Arrestin function in inactivation of G protein-coupled receptor rhodopsin in vivo.";
 RL Science 260:1910-1916(1993).
 CC -1- FUNCTION: Regulates photoreceptor cell deactivation. Arr1 and Arr2 proteins are mediators of rhodopsin inactivation and are essential for the termination of the phototransduction cascade.
 CC -1- INTERACTION:
 CC Q9VIM6:CG10949; NBExp=1; InAct=EBI-145156; EBI-153699;
 CC Q9VAP2:CG11881; NBExp=1; InAct=EBI-145156; EBI-186540;
 CC Q9V3Q2:CG12155; NBExp=1; InAct=EBI-145156; EBI-151453;
 CC Q9V7S6:CG37534; NBExp=1; InAct=EBI-145156; EBI-190361;
 CC Q9VTE0:CG33995; NBExp=1; InAct=EBI-145156; EBI-160250;
 CC Q9VTH5:CG6175; NBExp=1; InAct=EBI-145156; EBI-16076;
 CC Q9VH18:CG6254; NBExp=1; InAct=EBI-145156; EBI-125350;
 CC -1- TISSUE SPECIFICITY: Expressed specifically and abundantly in the photoreceptors. Inner and outer segments, and the inner plexiform regions of the retina.
 CC -1- PTM: Phosphorylated, but does not undergo light-induced phosphorylation.
 CC -1- SIMILARITY: Belongs to the arrestin family.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
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 CC EMBL: M30177; -; NOT ANNOTATED CDS; Genomic_DNA.
 CC EMBL: M30140; AAA28380.1; -; Genomic_DNA.
 CC EMBL: AE003657; AA83644.1; -; Genomic_DNA.
 CC EMBL: AY061824; AAL27635.1; -; mRNA.
 CC PIR: A34867; A34867.
 CC HSSP: P17870; 1G4M.
 CC InAct: P15372; -;
 CC Ensembl: CG5711; Drosophila melanogaster.
 CC FlyBase: FBgn000120; Arr1.
 CC BioCyc: DMEL-XXX-02:DMEL-XXX-02-009314-MONOMER; -;
 CC GO: GO:0005624; C:membrane fraction; IDA.
 CC GO: GO:0016028; C:rhodome; IDA.
 CC GO: GO:0005515; F:protein binding; IPI.
 CC GO: GO:0016060; P:metarhodopsin inactivation; IGI.
 CC InterPro: IPR000698; Arrestin.
 CC InterPro: IPR011022; Arrestin_C.


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DR InterPro; IPR011021; Arrestin_N.
DR PANTHER; PTHR11792; Arrestin; 1.
DR Pfam; PF02752; Arrestin_C; 1.
DR Pfam; PF00339; Arrestin_N; 1.
DR PRINTS; PR00309; ARRESTIN.
DR PRODOM; PD002099; ARRESTIN; 2.
DR PROSITE; PS00295; ARRESTIN; 1.
DR Complete proteome; Phosphorylation; Sensory transduction; Vision.
FT CHAIN 1 364 Phosrestin-2.
SQ SEQUENCE 364 AA; 40771 MW; 0DC6764C4F890FC2 CRC64;

Query Match 5.2%; Score 20; DB 1; Length 364;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 228 VKKIKAMVQGVVYLPONG 247
Db 227 VKKIKAMVQGVVYLPONG 246

RESULT 7
Q7YTV9 ANOST PRELIMINARY; PRT; 18 AA.
ID Q7YTV9 ANOST PRELIMINARY; PRT; 18 AA.
AC Q7YTV9;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Arrestin (Fragment).
GN Name=arr1;
OS Anopheles stephensi (Indo-Pakistan malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
OC Anophelinae; Anopheles; stephensi species complex.
OX NCBI_TaxID=30069;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Favia G., Ricci I., Casiraghi M., Esposito F.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AJ544226; CAD6651.1; -; Genomic_DNA.
DR NON TER 18
FT SEQUENCE 18 AA; 2075 MW; A273A394A2A6EF66 CRC64;
SQ

Query Match 4.7%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.5e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVYNFKVFKKCAPNGKVT 18
Db 1 MVYNFKVFKKCAPNGKVT 18

RESULT 8
Q7YTW0 9DIPT PRELIMINARY; PRT; 18 AA.
ID Q7YTW0 9DIPT PRELIMINARY; PRT; 18 AA.
AC Q7YTW0;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Arrestin (Fragment).
GN Name=arr1;
OS Anopheles pharocensis;
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=221566;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Favia G., Ricci I., Casiraghi M., Esposito F.;

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RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AJ544225; CAD6650.1; -; Genomic_DNA.
DR NON TER 18
FT SEQUENCE 18 AA; 2075 MW; A273A394A2A6EF66 CRC64;
SQ

Query Match 4.7%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.5e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVYNFKVFKKCAPNGKVT 18
Db 1 MVYNFKVFKKCAPNGKVT 18

RESULT 9
Q7YTW1 ANOAR PRELIMINARY; PRT; 18 AA.
ID Q7YTW1 ANOAR PRELIMINARY; PRT; 18 AA.
AC Q7YTW1;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Arrestin (Fragment).
GN Name=arr1;
OS Anopheles arabiensis (mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=7173;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Favia G., Ricci I., Casiraghi M., Esposito F.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AJ544224; CAD6649.1; -; Genomic_DNA.
DR NON TER 18
FT SEQUENCE 18 AA; 2075 MW; A273A394A2A6EF66 CRC64;
SQ

Query Match 4.7%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.5e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVYNFKVFKKCAPNGKVT 18
Db 1 MVYNFKVFKKCAPNGKVT 18

RESULT 10
ARR1 CALVI STANDARD; PRT; 363 AA.
ID ARR1 CALVI STANDARD; PRT; 363 AA.
AC P51486;
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-1996, sequence version 1.
DT 07-FEB-2006, entry version 28.
DE Phosrestin-2 (Phosrestin II) (Arrestin A) (Arrestin-1).
GN Name=ARR1;
OS Calliphora vicina (Blue blowfly) (Calliphora erythrocephala).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=7373;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RP TISSUE=Retina;
RX MEDLINE=95014564; PubMed=7929436;
RA Planger A., Malicki D., Whitney M., Paulsen R.;
RT "Mechanism of arrestin 2 function in rhabdomeric photoreceptors.";

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RL J. Biol. Chem. 269:26969-26975 (1994).
CC -1- SIMILARITY: Belongs to the arrestin family.
CC -----
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CC -----
DR EMBL: X79072; CAAS5672.1; -; mRNA.
DR PIR: A55081; A55081.
DR HSSP: P17870; 1G4M.
DR InterPro: IPR000698; Arrestin.
DR InterPro: IPR011022; Arrestin_C.
DR InterPro: IPR011021; Arrestin_N.
DR PANTHER: PTHR11792; Arrestin; 1.
DR Pfam: PF02752; Arrestin_C; 1.
DR Pfam: PF00339; Arrestin_N; 1.
DR PRINTS: PR00309; ARRESTIN.
DR PRODOM: PD02099; Arrestin; 2.
DR PROSITE: PS00295; ARRESTINS; 1.
KM Sensory transduction; Vision.
FT CHAIN 1 363
FT SEQUENCE 363 AA; 40680 MW; 7C345D818E46C23E CRC64;
SQ
Query Match 4.4%; Score 17; DB 1; Length 363;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 322 SYAVKVKFLGALGSEL 338
Db 321 SYAVKVKFLGALGSEL 337

RESULT 11
ARRH_HELVI STANDARD; PRT; 381 AA.
AC P55274;
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-1996, sequence version 1.
DT 07-FEB-2006, entry version 26.
DE Arrestin homolog.
OS Heliothis virescens (Noctuid moth) (Owlet moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditryaia; Noctuoidea;
OC Noctuidae; Heliothinae; Heliothis.
OX NCBI_TaxID=7102;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Antenna;
RX MEDLINE=93199955; PubMed=8452755; DOI=10.1016/0898-6568(93)90009-B;
RA Raming K., Freitag J., Krieger J., Breer H.;
RT "Arrestin-subtypes in insect antennae.";
RL Cell. Signal. 5:69-80(1993).
CC -1- SIMILARITY: Belongs to the arrestin family.
CC -----
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CC -----
DR PIR: B56607; B56607.
DR HSSP: P17870; 1G4M.
DR InterPro: IPR000698; Arrestin.
DR InterPro: IPR011022; Arrestin_C.
DR InterPro: IPR011021; Arrestin_N.
DR PANTHER: PTHR11792; Arrestin; 1.
DR Pfam: PF02752; Arrestin_C; 1.
DR Pfam: PF00339; Arrestin_N; 1.
DR PRINTS: PR00309; ARRESTIN.
DR PRODOM: PD02099; Arrestin; 2.
DR PROSITE: PS00295; ARRESTINS; 1.
KM Sensory transduction.
FT CHAIN 1 381
FT SEQUENCE 381 AA; 42747 MW; 84BB92B1BB3DA573 CRC64;
SQ

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Query Match 4.2%; Score 16; DB 1; Length 381;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MVTNFKYFKKCAPNGK 16
Db 1 MVTNFKYFKKCAPNGK 16

RESULT 12
Q6X126_DROYA PRELIMINARY; PRT; 52 AA.
ID Q6X126_DROYA
AC Q6X126;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Similar to Drosophila melanogaster CG5711 (Fragment).
DE Name=Arr1;
OS Drosophila yakuba (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7245;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22887302; PubMed=14525923; DOI=10.1101/gr.1311003;
RA Domazet-Loso T., Tautz D.;
RT "An evolutionary analysis of orphan genes in Drosophila.";
RL Genome Res. 13:2213-2219(2003).
CC -----
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CC -----
DR EMBL: AY232006; AAR10029.1; -; mRNA.
DR HSSP: P08168; 1AYR.
DR FLYbase: FBgn0068531; Dyak\Arr1.
DR GO: GO:0007600; P:sensory perception; IEA.
DR GO: GO:0007165; P:signal transduction; IEA.
DR InterPro: IPR000698; Arrestin.
DR InterPro: IPR011021; Arrestin_N.
DR PANTHER: PTHR11792; Arrestin; 1.
DR Pfam: PF00339; Arrestin_N; 1.
DR PRODOM: PD02099; Arrestin; 1.
FT NON_TER 1 1
FT NON_TER 52 52
SQ SEQUENCE 52 AA; 6166 MW; 081C148570B5EB6F CRC64;

Query Match 3.7%; Score 14; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 VEPIDGIVLDDEY 46
Db 33 VEPIDGIVLDDEY 46

RESULT 13
ARRH_LIMPO STANDARD; PRT; 400 AA.
ID ARR_H_LIMPO
AC P51484;
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-1996, sequence version 1.
DT 07-FEB-2006, entry version 26.
DE Arrestin, lateral eye.
OS Limulus polyphemus (Atlantic horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Limulus.
OX NCBI_TaxID=6850;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Retina;
RX MEDLINE=95096819; PubMed=7798902;
RA Smith W.C., Greenberg R.M., Calman B.G., Hendrix M.M., Hutchinson L.,

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RA Donoso L.A., Battelle B.-A.;
 RT "Isolation and expression of an arrestin cDNA from the horseshoe crab
 RT lateral eye."
 RL J. Neurochem. 64:1-13(1995).
 CC -1- FUNCTION: Plays an important role in the photoreceptor
 CC transduction.
 CC -1- PTM: Phosphorylated.
 CC -1- SIMILARITY: Belongs to the arrestin family.
 CC -----
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 CC -----
 CC EMBL, U08883; AA82007.1; -; mRNA.
 DR HSSP; P17870; IG4M.
 DR InterPro; IPR000698; Arrestin.
 DR InterPro; IPR011022; Arrestin_C.
 DR InterPro; IPR011021; Arrestin_N.
 DR PANTHER; PTHR11792; Arrestin; 1.
 DR Pfam; PF02752; Arrestin_C; 1.
 DR Pfam; PF00339; Arrestin_N; 1.
 DR PRINTS; PR00309; ARRESTIN.
 DR ProDom; PD002099; Arrestin; 2.
 DR PROSITE; PS00295; ARRESTINS; 1.
 DR Phosphorylation; Sensory transduction; Vision.
 KW CHAIN 1 400 Arrestin, lateral eye.
 FT /FTid=PRO_0000205219.
 FT SQ SEQUENCE 400 AA; 44302 MW; F3D0D025BC2BEE33 CRC64;
 FT
 Query Match 3.4%; Score 13; DB 1; Length 400;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 61 FRYGREDEVMGL 73
 |||||
 Db 68 FRYGREDEVMGL 80
 RESULT 14
 ID ARRH LOCMI STANDARD; PRT; 407 AA.
 AC P3122;
 DT 01-OCT-1993, integrated into UniProtKB/Swiss-Prot.
 DT 01-OCT-1993, sequence version 1.
 DT 07-FEB-2006, entry version 33.
 DE Arrestin homolog.
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OC NCBI_TaxID=7004;
 RX NUCLEOTIDE SEQUENCE [MRNA].
 RP TISSUE:Antenna;
 RC MEDLINE=9319955; PubMed=8452755; DOI=10.1016/0898-6568(93)90009-B;
 RA Raming K., Freitag J., Krieger J., Breer H.;
 RT "Arrestin-subtypes in insect antennae."
 RL Cell. Signal. 5:69-80(1993).
 CC -1- SIMILARITY: Belongs to the arrestin family.
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 CC -----
 CC EMBL, S57174; AAB25860.1; -; mRNA.
 DR PIR; A56607; A56607.
 DR HSSP; P17870; IG4M.
 DR InterPro; IPR000698; Arrestin.
 DR InterPro; IPR011022; Arrestin_C.
 DR InterPro; IPR011021; Arrestin_N.
 DR PANTHER; PTHR11792; Arrestin; 1.
 DR Pfam; PF02752; Arrestin_C; 1.
 DR Pfam; PF00339; Arrestin_N; 1.
 DR PRINTS; PR00309; ARRESTIN.
 DR ProDom; PD002099; Arrestin; 2.

DR PROSITE; PS00295; ARRESTINS; 1.
 KW Sensory transduction.
 RT CHAIN 1 407 Arrestin homolog.
 FT /FTid=PRO_0000205221.
 FT SQ SEQUENCE 407 AA; 45543 MW; DEC28A3A534935B CRC64;
 FT
 Query Match 3.1%; Score 12; DB 1; Length 407;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 62 RYGREDEVMGL 73
 |||||
 Db 69 RYGREDEVMGL 80
 RESULT 15
 ID O68D25 HUMAN PRELIMINARY; PRT; 217 AA.
 AC O68D25;
 DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
 DT 11-OCT-2004, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE Hypothetical protein DKFZp686L0365.
 DE Name=DKFZp686L0365;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RX NUCLEOTIDE SEQUENCE.
 RP TISSUE=Endometrium;
 RC The German cDNA Consortium;
 RA Ottenwälder B., Oberbauer B., Deutschenbaur S., Schaipp A.,
 RA Mewes H.W., Weil B., Amlid C., Osanger A., Fobo G., Han M., Wiemann S.;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
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 CC -----
 CC EMBL, CR749218; CAH18075.1; -; mRNA.
 DR SRR; O68D25; 1-169.
 DR Ensembl; ENSG00000141480; Homo sapiens.
 DR GO; GO:0007600; P:sensory perception; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000698; Arrestin.
 DR InterPro; IPR011022; Arrestin_C.
 DR PANTHER; PTHR11792; Arrestin; 1.
 DR Pfam; PF02752; Arrestin_C; 1.
 DR ProDom; PD002099; Arrestin; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 217 AA; 24363 MW; 61653F5BABCBB0FD CRC64;
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 OY 341 ELPFVLMHPKP 351
 |||||
 Db 147 ELPFVLMHPKP 157
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 Job time : 302 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 20, 2006, 23:15:44 ; Search time 49 Seconds
(without alignments)
684.168 Million cell updates/sec

Title: US-10-056-405-2

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	9	2.3	388	2	US-09-880-137-6
6	8	2.1	279	2	US-09-252-991A-27414
7	8	2.1	315	2	US-09-949-016-9940
8	8	2.1	401	2	US-09-949-016-8383
9	8	2.1	401	2	US-09-949-016-8384
10	8	2.1	418	2	US-09-880-137-1
11	8	2.1	418	2	US-09-880-137-2
12	8	2.1	418	2	US-09-641-528B-2512
13	8	2.1	418	2	US-09-641-528B-20553
14	8	2.1	418	2	US-09-641-528B-20552
15	8	2.1	418	2	US-09-641-528B-31963
16	8	2.1	418	2	US-09-641-528B-146
17	8	2.1	418	2	US-09-641-528B-2430
18	8	2.1	418	2	US-09-641-528B-20527
19	8	2.1	418	2	US-09-641-528B-20523
20	8	2.1	418	2	US-09-641-528B-31915
21	8	2.1	418	2	US-09-641-528B-31919
22	8	2.1	418	2	US-09-641-528B-20524
23	8	2.1	418	2	US-09-641-528B-20554
24	8	2.1	418	2	US-09-641-528B-31936
25	8	2.1	418	2	US-09-641-528B-31964
26	8	2.1	418	2	US-09-641-528B-147

27	7	1.8	11	3	US-09-641-528B-2490	Sequence 2490, Ap
28	7	1.8	11	3	US-09-641-528B-2513	Sequence 2513, Ap
29	7	1.8	11	3	US-09-641-528B-11937	Sequence 11937, A
30	7	1.8	11	3	US-09-641-528B-20525	Sequence 20525, A
31	7	1.8	11	3	US-09-641-528B-20528	Sequence 20528, A
32	7	1.8	11	3	US-09-641-528B-20555	Sequence 20555, A
33	7	1.8	11	3	US-09-641-528B-24797	Sequence 24797, A
34	7	1.8	11	3	US-09-641-528B-31920	Sequence 31920, A
35	7	1.8	11	3	US-09-641-528B-31952	Sequence 31952, A
36	7	1.8	15	1	US-08-484-905-28	Sequence 28, Appl
37	7	1.8	15	2	US-08-481-985B-28	Sequence 28, Appl
38	7	1.8	15	2	US-08-370-476-28	Sequence 8, Appl
39	7	1.8	15	2	US-08-992-877-8	Sequence 46501, A
40	7	1.8	15	3	US-09-641-528B-46501	Sequence 54, Appl
41	7	1.8	16	1	US-08-480-190-54	Sequence 54, Appl
42	7	1.8	16	1	US-08-488-379-54	Sequence 54, Appl
43	7	1.8	16	2	US-08-475-399A-54	Sequence 54, Appl
44	7	1.8	16	2	US-08-077-255A-54	Sequence 54, Appl
45	7	1.8	16	5	PCT-US93-07545-54	Sequence 54, Appl

ALIGNMENTS

RESULT 1
US-09-880-137-8
; Sequence 8, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: MNI-131
; CURRENT FILING DATE: US/09/880,137
; PRIOR APPLICATION NUMBER: 2001-03-05
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
US-09-880-137-8
Query Match 2.9%; Score 11; DB 2; Length 382;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 341 ELPPVLMHPKP 351
DB 339 ELPPVLMHPKP 349
RESULT 2
US-09-880-137-4
; Sequence 4, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: MNI-131
; CURRENT FILING DATE: US/09/880,137
; PRIOR APPLICATION NUMBER: 2001-03-05
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 409

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-137-4

Query Match
Best Local Similarity 100.0%; Score 11; DB 2; Length 409;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 ELFPVLMHMKP 351
DB 339 ELFPVLMHMKP 349

RESULT 3
US-09-880-137-7
; Sequence 7, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: MN1-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
US-09-880-137-7

Query Match
Best Local Similarity 100.0%; Score 11; DB 2; Length 409;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 ELFPVLMHMKP 351
DB 339 ELFPVLMHMKP 349

RESULT 4
US-09-880-137-5
; Sequence 5, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: MN1-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-137-5

Query Match
Best Local Similarity 100.0%; Score 9; DB 2; Length 388;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 GKRFVDHV 30
DB 19 GKRFVDHV 27

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-137-6

Query Match
Best Local Similarity 100.0%; Score 9; DB 2; Length 388;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 GKRFVDHV 30
DB 19 GKRFVDHV 27

RESULT 5
US-09-880-137-6
; Sequence 6, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: MN1-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-137-6

Query Match
Best Local Similarity 100.0%; Score 8; DB 2; Length 279;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 336 GELSAELP 343
DB 30 GELSAELP 37

RESULT 6
US-09-252-991A-27414
; Sequence 27414, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Maco J, Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27414
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27414

Query Match
Best Local Similarity 100.0%; Score 8; DB 2; Length 279;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 336 GELSAELP 343
DB 30 GELSAELP 37

RESULT 7
US-09-949-016-9940
; Sequence 9940, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
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;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 9940
;; LENGTH: 315
;; TYPE: PRT
;; ORGANISM: Human
US-09-949-016-9940

Query Match 2.1%; Score 8; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 GKRDFVDH 29
Db 24 GKRDFVDH 31

RESULT 8
US-09-949-016-8383
;; Sequence 8383, Application US/09949016
;; Patent No. 6812339
;; GENERAL INFORMATION:
;; APPLICANT: VENTER, J. Craig et al.
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; FILE REFERENCE: CL001307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 8383
;; LENGTH: 401
;; TYPE: PRT
;; ORGANISM: Human
US-09-949-016-8383

Query Match 2.1%; Score 8; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 GKRDFVDH 29
Db 6 GKRDFVDH 13

RESULT 9
US-09-949-016-8384
;; Sequence 8384, Application US/09949016
;; Patent No. 6812339
;; GENERAL INFORMATION:
;; APPLICANT: VENTER, J. Craig et al.
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; FILE REFERENCE: CL001307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03

;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 8384
;; LENGTH: 401
;; TYPE: PRT
;; ORGANISM: Human
US-09-949-016-8384

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Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 GKRDFVDH 29
Db 6 GKRDFVDH 13

RESULT 10
US-09-880-137-3
;; Sequence 3, Application US/09880137
;; Patent No. 6640025
;; GENERAL INFORMATION:
;; APPLICANT: Berstein, Gabriel
;; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
;; FILE REFERENCE: MNI-131
;; CURRENT APPLICATION NUMBER: US/09/880,137
;; PRIOR FILING DATE: 2001-03-05
;; PRIOR APPLICATION NUMBER: US 60/186,706
;; PRIOR FILING DATE: 2000-03-03
;; NUMBER OF SEQ ID NOS: 8
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 3
;; LENGTH: 410
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-137-3

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Best Local Similarity 100.0%; Pred. No. 31;
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Qy 22 GKRDFVDH 29
Db 23 GKRDFVDH 30

RESULT 11
US-09-880-137-1
;; Sequence 1, Application US/09880137
;; Patent No. 6640025
;; GENERAL INFORMATION:
;; APPLICANT: Berstein, Gabriel
;; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
;; FILE REFERENCE: MNI-131
;; CURRENT APPLICATION NUMBER: US/09/880,137
;; PRIOR FILING DATE: 2001-03-05
;; PRIOR APPLICATION NUMBER: US 60/186,706
;; PRIOR FILING DATE: 2000-03-03
;; NUMBER OF SEQ ID NOS: 8
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1
;; LENGTH: 418
;; TYPE: PRT
;; ORGANISM: Bos taurus
US-09-880-137-1

Query Match 2.1%; Score 8; DB 2; Length 418;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 GKRDVVDH 29
Db 23 GKRDVVDH 30

RESULT 12
US-09-880-137-2
; Sequence 2, Application US/099860137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: NMI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-137-2

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Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 22 GKRDVVDH 29
Db 23 GKRDVVDH 30

RESULT 13
US-09-641-528B-2512
; Sequence 2512, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2512
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-2512

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Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 303 ASTLLA 309
Db 2 ASTLLA 8

RESULT 14
US-09-641-528B-20553
; Sequence 20553, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20553
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-20553

Query Match 1.8%; Score 7; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 303 ASTLLA 309
Db 2 ASTLLA 8

RESULT 15
US-09-641-528B-31963
; Sequence 31963, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31963
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-31963

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Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 303 ASTLLA 309
Db 2 ASTLLA 8

Tue May 23 13:30:39 2006

us-10-056-405-2.011.rat

Page 5

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Job time : 50 secs

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GenCore version 5.1.8
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OM protein - protein search, using sw model

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Title: US-10-056-405-2

Perfect score: 383

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	383	100.0	383	4	US-10-056-405-2
3	383	100.0	383	5	US-10-954-778-238
4	20	5.2	364	5	US-10-745-237-18
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6	11	2.9	382	3	US-09-880-137-8
7	11	2.9	382	3	US-09-800-137A-8
8	11	2.9	398	4	US-10-094-240-25
9	11	2.9	398	4	US-10-954-778-241
10	11	2.9	401	4	US-10-094-240-27
11	11	2.9	401	6	US-11-097-143-12684
12	11	2.9	409	3	US-09-880-137-4
13	11	2.9	409	3	US-09-880-137-7
14	11	2.9	409	3	US-09-800-137A-4
15	11	2.9	409	3	US-09-800-137A-7
16	11	2.9	410	4	US-10-038-010-54
17	11	2.9	466	4	US-10-722-357-31
18	11	2.9	479	6	US-11-170-123-3
19	11	2.9	492	6	US-11-170-123-4
20	9	2.3	388	3	US-09-880-137-5
21	9	2.3	388	3	US-09-880-137-6
22	9	2.3	388	3	US-09-800-137A-5
23	9	2.3	388	3	US-09-800-137A-6
24	9	2.3	470	6	US-11-097-143-1314
25	8	2.1	38	3	US-09-864-761-40768
26	8	2.1	48	4	US-10-424-599-154582
27	8	2.1	63	4	US-10-425-115-191381

28	8	2.1	153	4	US-10-424-599-148204	Sequence 148204,
29	8	2.1	204	4	US-10-335-977-7580	Sequence 7580, Ap
30	8	2.1	208	4	US-10-767-701-41403	Sequence 41403, A
31	8	2.1	212	4	US-10-106-698-4673	Sequence 4673, Ap
32	8	2.1	235	4	US-10-424-599-224408	Sequence 224408,
33	8	2.1	235	6	US-11-087-099-1956	Sequence 1956, Ap
34	8	2.1	270	4	US-10-767-701-38282	Sequence 38282, A
35	8	2.1	307	4	US-10-425-115-244452	Sequence 244452,
36	8	2.1	366	4	US-10-335-977-7581	Sequence 7581, Ap
37	8	2.1	369	5	US-10-450-763-43933	Sequence 43933, A
38	8	2.1	410	3	US-09-880-137-3	Sequence 3,
39	8	2.1	410	3	US-09-800-137A-3	Sequence 1,
40	8	2.1	418	3	US-09-880-137-1	Sequence 1, Appli
41	8	2.1	418	3	US-09-880-137-2	Sequence 2, Appli
42	8	2.1	418	3	US-09-800-137A-2	Sequence 2, Appli
43	8	2.1	418	3	US-09-800-137A-2	Sequence 348, App
44	8	2.1	418	4	US-10-043-487-348	Sequence 216, App
45	8	2.1	418	5	US-10-745-237-216	

ALIGNMENTS

RESULT 1
US-10-094-240-2
Sequence 2, Application US/10094240
Publication No. US20030082637A1
GENERAL INFORMATION:
APPLICANT: ZWIBEL, LAURENCE J.
TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF
FILE REFERENCE: N8289
CURRENT APPLICATION NUMBER: US/10/094,240
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 10/056,405
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/264,649
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 383
TYPE: PRT
ORGANISM: Anopheles gambiae
US-10-094-240-2

Query Match	Best Local Similarity	Score	DB 4;	Length	383;
Matches	383;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;		
1	MYNFKVKFKCAPNGKVTLYMGKXDPVDHVGVEPIDGIVVLDDPYIRDNKRVFGQIVCS	60			
1	MYNFKVKFKCAPNGKVTLYMGKXDPVDHVGVEPIDGIVVLDDPYIRDNKRVFGQIVCS	60			
61	FRYGEDEWVGLNFKELCLASEQIYPRPEKSDKEQTKLOERLKLKLSNAIPTFNIS	120			
61	FRYGEDEWVGLNFKELCLASEQIYPRPEKSDKEQTKLOERLKLKLSNAIPTFNIS	120			
121	PNAPSVTLQOGEEDNPGCGVSYVVKIPAGESETRDTHRSSTVTLGIRKIOFAPATKQO	180			
121	PNAPSVTLQOGEEDNPGCGVSYVVKIPAGESETRDTHRSSTVTLGIRKIOFAPATKQO	180			
181	QCTTVRDPFMSPELELEVTLDKQYLHGERIGVNICIRNNSKMYKKIKAMVQOQVD	240			
181	QCTTVRDPFMSPELELEVTLDKQYLHGERIGVNICIRNNSKMYKKIKAMVQOQVD	240			
241	VVLFGNGSYRNTVASLETSEGCPIQPGSSLOKMYLTPRLSSNKORGIALDGOIKRODQ	300			
241	VVLFGNGSYRNTVASLETSEGCPIQPGSSLOKMYLTPRLSSNKORGIALDGOIKRODQ	300			
301	CLASTTLLAOPQORAFGVITISYANKVULFLGALGGEISAEIPFVLMHPKGTAKVHA	360			
301	CLASTTLLAOPQORAFGVITISYANKVULFLGALGGEISAEIPFVLMHPKGTAKVHA	360			

Qy 361 DSQADVFETFRDITDQASVDPE 383
Db 361 DSQADVFETFRDITDQASVDPE 383

RESULT 2

US-10-056-405-2
Sequence 2, Application US/10056405
Publication No. US20030166013A1
GENERAL INFORMATION:
APPLICANT: ZWIEBEL, LAURENCE J.
TITLE OF INVENTION: MOSQUITO OLEFACTORY GENES, POLYPEPTIDES, AND METHODS OF
FILE REFERENCE: N7841
CURRENT APPLICATION NUMBER: US/10/056,405
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/264,649
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 383
TYPE: PRT
ORGANISM: Anopheles gambiae
US-10-056-405-2

Query Match 100.0%; Score 383; DB 4; Length 383;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVYVFKVKKCAPNGKVTLYMGKRFVDHVGVEPIDGIIVLDDDEYIRDNKRVFGQIVCS 60
Db 1 MVYVFKVKKCAPNGKVTLYMGKRFVDHVGVEPIDGIIVLDDDEYIRDNKRVFGQIVCS 60
Qy 61 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNALPFTNIS 120
Db 61 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNALPFTNIS 120
Qy 121 PNAASSVTLLQGGEDNDGPPCGVSYVVKIFAGESETDRTHRSVTYLGIRKIQFAPTKQGO 180
Db 121 PNAASSVTLLQGGEDNDGPPCGVSYVVKIFAGESETDRTHRSVTYLGIRKIQFAPTKQGO 180
Qy 181 QPCTLVKRDPMLSPEGELEVTLDKQLYLHGERIGVNICIRNNSNKVKKIKAMVQOGVD 240
Db 181 QPCTLVKRDPMLSPEGELEVTLDKQLYLHGERIGVNICIRNNSNKVKKIKAMVQOGVD 240
Qy 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKORRGIALDGOIKRODQ 300
Db 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKORRGIALDGOIKRODQ 300
Qy 301 CLASTTLLAQPDRAPAGVITISYAVKVLFLGALGELSALPVLMPKPGTKAKVIHA 360
Db 301 CLASTTLLAQPDRAPAGVITISYAVKVLFLGALGELSALPVLMPKPGTKAKVIHA 360
Qy 361 DSQADVFETFRDITDQASVDPE 383
Db 361 DSQADVFETFRDITDQASVDPE 383

RESULT 3

US-10-954-778-238
Sequence 238, Application US/10954778
Publication No. US2005015368A1
GENERAL INFORMATION:
APPLICANT: ZWIEBEL, LAURENCE J.
TITLE OF INVENTION: METHOD OF IDENTIFYING CHEMICAL AGENTS WHICH STIMULATE
FILE REFERENCE: N1125
CURRENT APPLICATION NUMBER: US/10/954,778
CURRENT FILING DATE: 2004-09-30
PRIOR APPLICATION NUMBER: 10/056,405
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/264,649

PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 248
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 238
LENGTH: 383
TYPE: PRT
ORGANISM: Anopheles gambiae
US-10-954-778-238

Query Match 100.0%; Score 383; DB 5; Length 383;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVYVFKVKKCAPNGKVTLYMGKRFVDHVGVEPIDGIIVLDDDEYIRDNKRVFGQIVCS 60
Db 1 MVYVFKVKKCAPNGKVTLYMGKRFVDHVGVEPIDGIIVLDDDEYIRDNKRVFGQIVCS 60
Qy 61 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNALPFTNIS 120
Db 61 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNALPFTNIS 120
Qy 121 PNAASSVTLLQGGEDNDGPPCGVSYVVKIFAGESETDRTHRSVTYLGIRKIQFAPTKQGO 180
Db 121 PNAASSVTLLQGGEDNDGPPCGVSYVVKIFAGESETDRTHRSVTYLGIRKIQFAPTKQGO 180
Qy 181 QPCTLVKRDPMLSPEGELEVTLDKQLYLHGERIGVNICIRNNSNKVKKIKAMVQOGVD 240
Db 181 QPCTLVKRDPMLSPEGELEVTLDKQLYLHGERIGVNICIRNNSNKVKKIKAMVQOGVD 240
Qy 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKORRGIALDGOIKRODQ 300
Db 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKORRGIALDGOIKRODQ 300
Qy 301 CLASTTLLAQPDRAPAGVITISYAVKVLFLGALGELSALPVLMPKPGTKAKVIHA 360
Db 301 CLASTTLLAQPDRAPAGVITISYAVKVLFLGALGELSALPVLMPKPGTKAKVIHA 360
Qy 361 DSQADVFETFRDITDQASVDPE 383
Db 361 DSQADVFETFRDITDQASVDPE 383

RESULT 4

US-10-745-237-18
Sequence 18, Application US/10745237
Publication No. US20050227301A1
GENERAL INFORMATION:
APPLICANT: Cyclocel Limited
APPLICANT: Glover, David
APPLICANT: Bell, Graham
APPLICANT: Frenz, Lisa
APPLICANT: Migley, Carol
TITLE OF INVENTION: Cell Cycle Progression Proteins
FILE REFERENCE: P015819WO CYK
CURRENT APPLICATION NUMBER: US/10/745,237
CURRENT FILING DATE: 2003-12-23
PRIOR APPLICATION NUMBER: US 60/439,123
PRIOR FILING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: US 60/468,402
NUMBER OF SEQ ID NOS: 600
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 364
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: AAF53644
FEATURE:
OTHER INFORMATION: GI:7298421
US-10-745-237-18

Query Match 5.2%; Score 20; DB 5; Length 364;

Best Local Similarity 100.0%; Pred. No. 3.4e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 VKKIKAMVQGVVLFQNG 247
Db 227 VKKIKAMVQGVVLFQNG 246

RESULT 5
US-11-097-143-12000

; Sequence 12000, Application US/11097143
; Publication No. US20050208558A1

; GENERAL INFORMATION:

; APPLICANT: Venter, J. Craig

; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

; FILE REFERENCE: DROSOPHILA GENES.

; CURRENT APPLICATION NUMBER: US/11/097,143

; CURRENT FILING DATE: 2005-04-04

; PRIOR APPLICATION NUMBER: 60/157,832

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: 60/160,191

; PRIOR FILING DATE: 1999-10-19

; PRIOR APPLICATION NUMBER: 60/161,932

; PRIOR FILING DATE: 1999-10-28

; PRIOR APPLICATION NUMBER: 60/164,769

; PRIOR FILING DATE: 1999-11-12

; PRIOR APPLICATION NUMBER: 60/173,383

; PRIOR FILING DATE: 1999-12-28

; PRIOR APPLICATION NUMBER: 60/175,693

; PRIOR FILING DATE: 2000-01-12

; PRIOR APPLICATION NUMBER: 60/184,831

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: 60/191,637

; PRIOR FILING DATE: 2000-03-23

; NUMBER OF SEQ ID NOS: 43008

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12000

; LENGTH: 364

; TYPE: PRT

; ORGANISM: DROSOPHILA

US-11-097-143-12000

Query Match 5.2%; Score 20; DB 6; Length 364;
Best Local Similarity 100.0%; Pred. No. 3.4e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 VKKIKAMVQGVVLFQNG 247
Db 227 VKKIKAMVQGVVLFQNG 246

RESULT 6
US-09-880-137-8

; Sequence 8, Application US/09880137

; Patent No. US20020031295A1

; GENERAL INFORMATION:

; APPLICANT: Berstein, Gabriel

; TITLE OF INVENTION: METHODS OF ASSAYING FOR G

; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS

; FILE REFERENCE: MNI-131

; CURRENT APPLICATION NUMBER: US/09/880,137

; CURRENT FILING DATE: 2001-03-05

; PRIOR APPLICATION NUMBER: US 60/186,706

; PRIOR FILING DATE: 2000-03-03

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 8

; LENGTH: 382

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
US-09-880-137-8

Query Match 2.9%; Score 11; DB 3; Length 382;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 ELFPVLMHPKP 351
Db 339 ELFPVLMHPKP 349

RESULT 7

US-09-800-137A-8

; Sequence 8, Application US/09800137A

; Publication No. US20030157553A1

; GENERAL INFORMATION:

; APPLICANT: Berstein, Gabriel

; TITLE OF INVENTION: METHODS OF ASSAYING FOR G

; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS

; FILE REFERENCE: MNI-131

; CURRENT APPLICATION NUMBER: US/09/800,137A

; CURRENT FILING DATE: 2001-03-05

; PRIOR APPLICATION NUMBER: US 60/186,706

; PRIOR FILING DATE: 2000-03-03

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 8

; LENGTH: 382

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
US-09-800-137A-8

Query Match 2.9%; Score 11; DB 3; Length 382;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 ELFPVLMHPKP 351
Db 339 ELFPVLMHPKP 349

RESULT 8
US-10-094-240-25

; Sequence 25, Application US/10094240

; Publication No. US20030082637A1

; GENERAL INFORMATION:

; APPLICANT: ZWITBEL, LAURENCE J.

; TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF

; FILE REFERENCE: N8289

; CURRENT APPLICATION NUMBER: US/10/094,240

; CURRENT FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: 10/056,405

; PRIOR FILING DATE: 2002-01-24

; PRIOR APPLICATION NUMBER: 60/264,649

; PRIOR FILING DATE: 2001-01-26

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 25

; LENGTH: 398

; TYPE: PRT

; ORGANISM: Anopheles gambiae

US-10-094-240-25

Query Match 2.9%; Score 11; DB 4; Length 398;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 RYGREDEVMG 72
|||||

Db 61 RYGREDEVMG 71

RESULT 9
US-10-954-778-241

; Sequence 241, Application US/10954778
; Publication No. US2005015368A1

; GENERAL INFORMATION:

; APPLICANT: ZWIEBEL, LAURENCE J.

; TITLE OF INVENTION: METHOD OF IDENTIFYING CHEMICAL AGENTS WHICH STIMULATE
; TITLE OF INVENTION: ODORANT RECEPTORS OF SENSORY NEURONS

; FILE REFERENCE: N1125

; CURRENT APPLICATION NUMBER: US/10/954,778

; CURRENT FILING DATE: 2004-09-30

; PRIOR APPLICATION NUMBER: 10/056,405

; PRIOR FILING DATE: 2002-01-24

; PRIOR APPLICATION NUMBER: 60/264,649

; PRIOR FILING DATE: 2001-01-26

; NUMBER OF SEQ ID NOS: 248

; SOFTWARE: PatentIn Ver. 3.3

; SEQ ID NO 241

; LENGTH: 398

; TYPE: PRT

; ORGANISM: Anopheles gambiae

US-10-954-778-241

Query Match 2.9%; Score 11; DB 5; Length 398;
Best Local Similarity 100.0%; Pred. No. 0.16;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 RYGREDEVMG 72
|||||
Db 61 RYGREDEVMG 71

RESULT 10
US-10-094-240-27

; Sequence 27, Application US/10094240
; Publication No. US20030082637A1

; GENERAL INFORMATION:

; APPLICANT: ZWIEBEL, LAURENCE J.

; TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF

; FILE REFERENCE: N8289

; CURRENT APPLICATION NUMBER: US/10/094,240

; CURRENT FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: 10/056,405

; PRIOR FILING DATE: 2002-01-24

; PRIOR APPLICATION NUMBER: 60/264,649

; PRIOR FILING DATE: 2001-01-26

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 27

; LENGTH: 401

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

US-10-094-240-27

Query Match 2.9%; Score 11; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 0.16;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 RYGREDEVMG 72
|||||
Db 61 RYGREDEVMG 71

RESULT 11
US-11-097-143-12684

; Sequence 12684, Application US/11097143
; Publication No. US20050208558A1

; GENERAL INFORMATION:

; APPLICANT: Venter, J. Craig
; APPLICANT: et al.

; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.

; FILE REFERENCE: C1000728

; CURRENT APPLICATION NUMBER: US/11/097,143

; CURRENT FILING DATE: 2005-04-04

; PRIOR APPLICATION NUMBER: 60/157,832

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: 60/160,191

; PRIOR FILING DATE: 1999-10-19

; PRIOR APPLICATION NUMBER: 60/161,932

; PRIOR FILING DATE: 1999-10-28

; PRIOR APPLICATION NUMBER: 60/164,769

; PRIOR FILING DATE: 1999-11-12

; PRIOR APPLICATION NUMBER: 60/173,383

; PRIOR FILING DATE: 1999-12-28

; PRIOR APPLICATION NUMBER: 60/175,693

; PRIOR FILING DATE: 2000-01-12

; PRIOR APPLICATION NUMBER: 60/184,831

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: 60/191,637

; PRIOR FILING DATE: 2000-03-23

; NUMBER OF SEQ ID NOS: 43008

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12684

; LENGTH: 401

; TYPE: PRT

; ORGANISM: DROSOPHILA

US-11-097-143-12684

Query Match 2.9%; Score 11; DB 6; Length 401;
Best Local Similarity 100.0%; Pred. No. 0.16;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 RYGREDEVMG 72
|||||
Db 61 RYGREDEVMG 71

RESULT 12
US-09-880-137-4

; Sequence 4, Application US/09880137
; Patent No. US20020031295A1

; GENERAL INFORMATION:

; APPLICANT: Berstein, Gabriel

; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS

; FILE REFERENCE: WNI-131

; CURRENT APPLICATION NUMBER: US/09/880,137

; CURRENT FILING DATE: 2001-03-05

; PRIOR APPLICATION NUMBER: US 60/186,706

; PRIOR FILING DATE: 2000-03-03

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 409

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-880-137-4

Query Match 2.9%; Score 11; DB 3; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.16;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 ELFPVLMHMKP 351
|||||
Db 339 ELFPVLMHMKP 349

RESULT 13
US-09-880-137-7

; Sequence 7, Application US/09880137
; Patent No. US20020031295A1

```
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: MNT-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 7
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
US-09-880-137-7

Query Match      2.9%; Score 11; DB 3; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      341 ELPFVLMHPRK 351
        |||||
DB      339 ELPFVLMHPRK 349

RESULT 14
US-09-800-137A-4
; Sequence 4, Application US/09800137A
; Publication No. US20030157553A1
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: MNT-131
; CURRENT APPLICATION NUMBER: US/09/800,137A
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 4
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-137A-4

Query Match      2.9%; Score 11; DB 3; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      341 ELPFVLMHPRK 351
        |||||
DB      339 ELPFVLMHPRK 349

RESULT 15
US-09-800-137A-7
; Sequence 7, Application US/09800137A
; Publication No. US20030157553A1
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: MNT-131
; CURRENT APPLICATION NUMBER: US/09/800,137A
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO: 7
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
US-09-800-137A-7

Query Match      2.9%; Score 11; DB 3; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      341 ELPFVLMHPRK 351
        |||||
DB      339 ELPFVLMHPRK 349

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OM protein - protein search, using sw model

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(without alignments)
81.813 Million cell updates/sec

Title: US-10-056-405-2

Perfect score: 383

Sequence: 1 MVINPKVFKKCAPNGKVTLY.....ADVFTRDITDQASVDFE 383

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 21570 seqs, 2136119 residues

Word size : 1

Total number of hits satisfying chosen parameters: 21565

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database : Published Applications AA New:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	2.9	409	6	US-10-505-928-173
2	7	1.8	709	7	US-11-258-767-31
3	7	1.8	710	7	US-11-258-767-33
4	7	1.8	711	7	US-11-258-767-12
5	7	1.8	711	7	US-11-258-767-15
6	7	1.8	711	7	US-11-258-767-17
7	7	1.8	711	7	US-11-258-767-18
8	7	1.8	711	7	US-11-258-767-21
9	7	1.8	711	7	US-11-258-767-27
10	7	1.8	711	7	US-11-258-767-30
11	7	1.8	711	7	US-11-258-767-34
12	7	1.8	993	6	US-10-511-937-2463
13	6	1.6	34	6	US-10-706-435A-24
14	6	1.6	130	6	US-10-370-959-30
15	6	1.6	142	6	US-10-511-937-2437
16	6	1.6	178	6	US-10-196-749-464
17	6	1.6	283	7	US-11-106-014-50
18	6	1.6	353	7	US-11-117-196-11
19	6	1.6	363	6	US-10-511-937-2458
20	6	1.6	363	6	US-10-511-937-2994
21	6	1.6	411	7	US-11-254-182-47
22	6	1.6	419	7	US-11-302-678-44
23	6	1.6	440	7	US-11-254-182-49
24	6	1.6	456	6	US-10-706-435A-26
25	6	1.6	457	6	US-10-706-435A-4

26	6	1.6	467	6	US-10-511-937-2961	Sequence 2961, Ap
27	6	1.6	493	7	US-11-312-958-22	Sequence 22, Appl
28	6	1.6	544	6	US-10-505-928-859	Sequence 859, App
29	6	1.6	578	6	US-10-523-014-6	Sequence 6, Appl
30	6	1.6	590	7	US-11-106-014-52	Sequence 52, Appl
31	6	1.6	591	6	US-10-505-928-632	Sequence 632, App
32	6	1.6	615	7	US-11-248-122-4	Sequence 4, Appl
33	6	1.6	659	6	US-10-511-937-2593	Sequence 2593, Ap
34	6	1.6	694	6	US-10-505-928-288	Sequence 288, App
35	6	1.6	720	6	US-10-505-928-2423	Sequence 2423, Ap
36	6	1.6	976	6	US-10-511-455-2	Sequence 2, Appl
37	6	1.6	1066	6	US-10-505-928-175	Sequence 175, App
38	6	1.6	1085	6	US-11-248-122-2	Sequence 2, Appl
39	6	1.6	1308	7	US-11-248-122-2	Sequence 2545, Ap
40	6	1.6	1539	6	US-10-512-386-56	Sequence 56, Appl
41	6	1.6	1924	6	US-10-525-126-20	Sequence 20, Appl
42	5	1.3	7	6	US-10-490-949-9	Sequence 9, Appl
43	5	1.3	15	6	US-11-326-265-20	Sequence 20, Appl
44	5	1.3	19	7	US-11-176-182-104	Sequence 104, App
45	5	1.3	20	7		

ALIGNMENTS

```
RESULT 1
US-10-505-928-173
; Sequence 173, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; PRIOR FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 173
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-173

Query Match      2.9%; Score 11; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      341 ELPPVLMHMKP 351
DB      339 ELPPVLMHMKP 349

RESULT 2
US-11-258-767-31
; Sequence 31, Application US/11258767
; Publication No. US20060094082A1
; GENERAL INFORMATION:
; APPLICANT: Varadhachary, Atul
; APPLICANT: Glynn, Peter
; APPLICANT: Petrak, Karel
; APPLICANT: Engelmyer, Jose
; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
; FILE REFERENCE: HO-P02915US1
; CURRENT APPLICATION NUMBER: US/11/258,767
; PRIOR FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/622,176
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31
; LENGTH: 709
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TYPE: PRT
ORGANISM: HUMAN
US-11-258-767-31

Query Match 1.8%; Score 7; DB 7; Length 709;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 329 LFLGALG 335
DB 7 LFLGALG 13

RESULT 3
US-11-258-767-33
Sequence 33, Application US/11258767
Publication No. US20060094082A1
GENERAL INFORMATION:
APPLICANT: Varadhachary, Atul
APPLICANT: Glynn, Peter
APPLICANT: Petrak, Karel
APPLICANT: Engelmayr, Jose
TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
FILE REFERENCE: HO-P02915US1
CURRENT APPLICATION NUMBER: US/11/258,767
CURRENT FILING DATE: 2005-10-26
PRIOR APPLICATION NUMBER: US 60/622,176
PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.3
SEQ ID NO 33
LENGTH: 710
TYPE: PRT
ORGANISM: HUMAN
US-11-258-767-33

Query Match 1.8%; Score 7; DB 7; Length 710;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 329 LFLGALG 335
DB 9 LFLGALG 15

RESULT 4
US-11-258-767-12
Sequence 12, Application US/11258767
Publication No. US20060094082A1
GENERAL INFORMATION:
APPLICANT: Varadhachary, Atul
APPLICANT: Glynn, Peter
APPLICANT: Petrak, Karel
APPLICANT: Engelmayr, Jose
TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
FILE REFERENCE: HO-P02915US1
CURRENT APPLICATION NUMBER: US/11/258,767
CURRENT FILING DATE: 2005-10-26
PRIOR APPLICATION NUMBER: US 60/622,176
PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.3
SEQ ID NO 12
LENGTH: 711
TYPE: PRT
ORGANISM: HUMAN
US-11-258-767-12

Query Match 1.8%; Score 7; DB 7; Length 711;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 329 LFLGALG 335

DB 9 LFLGALG 15

RESULT 5
US-11-258-767-15
Sequence 15, Application US/11258767
Publication No. US20060094082A1
GENERAL INFORMATION:
APPLICANT: Varadhachary, Atul
APPLICANT: Glynn, Peter
APPLICANT: Petrak, Karel
APPLICANT: Engelmayr, Jose
TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
FILE REFERENCE: HO-P02915US1
CURRENT APPLICATION NUMBER: US/11/258,767
CURRENT FILING DATE: 2005-10-26
PRIOR APPLICATION NUMBER: US 60/622,176
PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.3
SEQ ID NO 15
LENGTH: 711
TYPE: PRT
ORGANISM: HUMAN
US-11-258-767-15

Query Match 1.8%; Score 7; DB 7; Length 711;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 329 LFLGALG 335
DB 9 LFLGALG 15

RESULT 6
US-11-258-767-17
Sequence 17, Application US/11258767
Publication No. US20060094082A1
GENERAL INFORMATION:
APPLICANT: Varadhachary, Atul
APPLICANT: Glynn, Peter
APPLICANT: Petrak, Karel
APPLICANT: Engelmayr, Jose
TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
FILE REFERENCE: HO-P02915US1
CURRENT APPLICATION NUMBER: US/11/258,767
CURRENT FILING DATE: 2005-10-26
PRIOR APPLICATION NUMBER: US 60/622,176
PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.3
SEQ ID NO 17
LENGTH: 711
TYPE: PRT
ORGANISM: HUMAN
US-11-258-767-17

Query Match 1.8%; Score 7; DB 7; Length 711;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 329 LFLGALG 335
DB 9 LFLGALG 15

RESULT 7
US-11-258-767-18
Sequence 18, Application US/11258767
Publication No. US20060094082A1
GENERAL INFORMATION:

APPLICANT: Varadhachary, Atul
APPLICANT: Glynn, Peter
APPLICANT: Petrak, Karel
APPLICANT: Engelmayr, Jose
TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
FILE REFERENCE: HO-P02915US1
CURRENT APPLICATION NUMBER: US/11/258,767
CURRENT FILING DATE: 2005-10-26
PRIOR APPLICATION NUMBER: US 60/622,176
PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.3
SEQ ID NO 18
LENGTH: 711
TYPE: PRT
ORGANISM: HUMAN
US-11-258-767-18

Query Match 1.8%; Score 7; DB 7; Length 711;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 329 LFLGALG 335
DB 9 LFLGALG 15

RESULT 8
US-11-258-767-21
Sequence 21, Application US/11258767
Publication No. US20060094082A1
GENERAL INFORMATION:
APPLICANT: Varadhachary, Atul
APPLICANT: Glynn, Peter
APPLICANT: Petrak, Karel
APPLICANT: Engelmayr, Jose
TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
FILE REFERENCE: HO-P02915US1
CURRENT APPLICATION NUMBER: US/11/258,767
CURRENT FILING DATE: 2005-10-26
PRIOR APPLICATION NUMBER: US 60/622,176
PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.3
SEQ ID NO 21
LENGTH: 711
TYPE: PRT
ORGANISM: HUMAN
US-11-258-767-21

Query Match 1.8%; Score 7; DB 7; Length 711;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 329 LFLGALG 335
DB 9 LFLGALG 15

RESULT 9
US-11-258-767-27
Sequence 27, Application US/11258767
Publication No. US20060094082A1
GENERAL INFORMATION:
APPLICANT: Varadhachary, Atul
APPLICANT: Glynn, Peter
APPLICANT: Petrak, Karel
APPLICANT: Engelmayr, Jose
TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
FILE REFERENCE: HO-P02915US1
CURRENT APPLICATION NUMBER: US/11/258,767
CURRENT FILING DATE: 2005-10-26
PRIOR APPLICATION NUMBER: US 60/622,176

PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.3
SEQ ID NO 27
LENGTH: 711
TYPE: PRT
ORGANISM: HUMAN
US-11-258-767-27

Query Match 1.8%; Score 7; DB 7; Length 711;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 329 LFLGALG 335
DB 9 LFLGALG 15

RESULT 10
US-11-258-767-30
Sequence 30, Application US/11258767
Publication No. US20060094082A1
GENERAL INFORMATION:
APPLICANT: Varadhachary, Atul
APPLICANT: Glynn, Peter
APPLICANT: Petrak, Karel
APPLICANT: Engelmayr, Jose
TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
FILE REFERENCE: HO-P02915US1
CURRENT APPLICATION NUMBER: US/11/258,767
CURRENT FILING DATE: 2005-10-26
PRIOR APPLICATION NUMBER: US 60/622,176
PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.3
SEQ ID NO 30
LENGTH: 711
TYPE: PRT
ORGANISM: HUMAN
US-11-258-767-30

Query Match 1.8%; Score 7; DB 7; Length 711;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 329 LFLGALG 335
DB 9 LFLGALG 15

RESULT 11
US-11-258-767-34
Sequence 34, Application US/11258767
Publication No. US20060094082A1
GENERAL INFORMATION:
APPLICANT: Varadhachary, Atul
APPLICANT: Glynn, Peter
APPLICANT: Petrak, Karel
APPLICANT: Engelmayr, Jose
TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
FILE REFERENCE: HO-P02915US1
CURRENT APPLICATION NUMBER: US/11/258,767
CURRENT FILING DATE: 2005-10-26
PRIOR APPLICATION NUMBER: US 60/622,176
PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.3
SEQ ID NO 34
LENGTH: 711
TYPE: PRT
ORGANISM: HUMAN
US-11-258-767-34

Query Match 1.8%; Score 7; DB 7; Length 711;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 329 LFLGALG 335
Db 9 LFLGALG 15

RESULT 12

US-10-511-937-2463
; Sequence 2463, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: US/10/511,937
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2463
; LENGTH: 993
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2463

Query Match 1.8%; Score 7; DB 6; Length 993;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 50 NRKVFQ 56
Db 488 NRKVFQ 494

RESULT 13

US-10-706-435A-24
; Sequence 24, Application US/10706435A
; Publication No. US20060088547A1
; GENERAL INFORMATION:
; APPLICANT: Walter Reed Army Institute of Research
; APPLICANT: Lanier, David E.
; APPLICANT: Hillier, Collette J.
; APPLICANT: Lyon, Jeffrey A.
; APPLICANT: Angov, Evelina
; APPLICANT: Kumar, Sanjai
; APPLICANT: Rogers, William
; APPLICANT: Barbosa, Arnoldo
; TITLE OF INVENTION: Expression, Purification, and Uses of a Plasmodium
; FILE REFERENCE: 003/285/SAP
; CURRENT APPLICATION NUMBER: US/10/706,435A
; PRIOR FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 60/425,719
; PRIOR FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Word XP
; SEQ ID NO 24

; LENGTH: 34
; TYPE: PRT
; ORGANISM: P. falciparum USA-1
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of USA-NRCH repeat sequence
US-10-706-435A-24

Query Match 1.6%; Score 6; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 99 KLGRL 104
Db 15 KLGRL 20

RESULT 14

US-10-370-959-30
; Sequence 30, Application US/10370959
; Publication No. US20060088907A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark W.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Hunter, John J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Bandaru, Rajasekhar
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: NOVEL 1237, 18480, 2245, 16228, 7677,
; TITLE OF INVENTION: 2630, 46619, 33166, 16836, 46867, 21617, 55562, 39228,
; TITLE OF INVENTION: 62088, 46745, 23155, 21657, 42755, 33229, 22325, 46863 AND
; TITLE OF INVENTION: 32252 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-01/OWNIM
; CURRENT APPLICATION NUMBER: US/10/370,959
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 09/910,150
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/219,028
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 10/251,507
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 09/715,479
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/218,053
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: US 09/644,929
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: US 60/212,439
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 09/892,870
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,174
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 09/775,117
; PRIOR FILING DATE: 2001-02-01
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid sequence
US-10-370-959-30

Query Match 1.6%; Score 6; DB 6; Length 130;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 104 LKKLG 109
|||
Db 3 LKKLG 8

RESULT 15

US-10-511-937-2437
; Sequence 2437, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2437
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2437

Query Match 1.6%; Score 6; DB 6; Length 142;
Best local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 106 KKLGSN 111
|||
Db 16 KKLGSN 21

Search completed: May 20, 2006, 23:11:05
Job time : 10 secs

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